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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                            September 16, 2003, 17:35:29; Search time 723.713 Seconds (without alignments) 1865.405 Million cell updates/sec
    2888711 seqs, 20454813386 residues
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33
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Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 64.8 | 4 | | 64.8 | 64.8 | .4 | | | 64.8 | 6.1 | 6.1 | 6.1 | 7. | 67.9 | 7. | 7. | 7 | 0 | œ : | 90 9 | D 0 | • | 68.5 | æ | œ | œ | œ | œ | 68.5 | 'n | Match | * |
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| E03113 | E03025 | HS1GBP | 361 | 108686 | BD165794 | B03112 | E03092 | E03024 | E01195 | E00883 | E03115 | AF259899 | HHU49121 | AF311740 | AF097023 | BD165795 | BD145144 | E03093 | _ | 865444 | S74390 | 103657 | AC133576 | AC140469 | OSJN00141 | CNS01DS7 | AF214736 | 3310 | AR308082 | AF181264 | HSV2HG52 | HS2GB2A | HOO | 108685 | HSZGB | ទេ | HHU12173 | HHU12174 | HHU12172 | .AF021340 | BD145143 | BD165793 | ⊳ | ä | |
| 03113 DNA | 25 DNA encodi | 4 | 61 Seque | 86 Sequence | 579 | 12 DNA encodi | 92 DNA | DNA | U | E00883 Fragment of | DNA | AF259899 Human her | duman he | Human | 3 Human h | D165795 Vaccine | 7 | 3 DNA en | 0 HSV1 (muta | 4 | 0 | 7 Sequen | 76 Mus | 69 Mus musc | 45 Oryz | 57 BAC sequ | 36 Homo | 0 | 308082 Sequence | 4 Homo s | 9 Herbes | 1 Herbes sim | TSILA HEV-2 (3 | Semial | M14923 1 | 5 Humai | 3 Human | 4 Human | Human herp | 0 Human h | 3 Herpes s | BD165793 Vaccine f | 112273 Mus mus | ; | |

ALIGNMENTS

| TITLE JOURNAL | AUTHORS | REFERENCE | | ORGANISM | SOURCE | KEYWORDS | VERSION | ACCESSION | DEFINITION | Locus | AC112273 | RESULT 1 |
|--|-------------------------------------|--|---|--------------|----------------------------|----------|------------------------|------------|--|---|----------|----------|
| The sequence of Mus musculus clone Unpublished | McPherson, J.D. and Waterston, R.H. | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 180155) | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | Mus musculus | Mus musculus (house mouse) | HTG. | AC112273.4 GI:22539282 | AC112273 . | Mus musculus chromosome 3 clone RP24-122H5, complete sequence. | AC112273 180155 bp DNA linear ROD 29-AUG-2002 | | |

Pred. No.

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                                                             Patent: JP 2002167398-A 2 11-JUN-2002;
CHIRON CORP
OS Herpes simplex virus 7
OS Herpes simplex virus 7
PN JP 2002167398-A/2
PD 11-JUN-2002
PP 11-SEP-2001 JP 2001277340
PR 20-OCT-1986 US 921.213
PR 20-OCT-1986 US 921.213
PI RAE LYN BURKE, CAROL PACHL, PABLO D T VALENZUELA PC COTK14/035, A61K39/245, A61P31/22, C12N15/09, C12N15/09, C12N15/00, C12N15/00
CC Vaccine for use in the therapeutic treatment of HSV FH K
                                                                                                                                                                                                                                               Herpes simplex virus 7
Herpes simplex virus 7
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 2712)
Burke, R.L., Pachl, C. and Valenzuela, P.D.T.
Vaccine for use in the thorapeutic treatment of HSV
Patent: JP 2002167398-A 2 11-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                            BD165793
BD165793.1 GI:278
JP 2002167398-A/2.
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Submitted (29-AUG-2002) Genome Sequencing Center, 4444 Fore
Parkway, St. Louis, MO 63108, USA
On Aug 29, 2002 this sequence version replaced gi:21240758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-MAY-2002) Genome Sequencing Center, Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 180155)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 180155)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 180155)
McPherson, J.D. and Wat
Direct Submission
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Contact: submissions@watson.wustl.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center code: WUGSC
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Submitted (20-FEB-2002) Genome Sequencing Center, 4444 Forest Park
                                   3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BD165793
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              Location/Qualifiers
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/mol_type="genomic DNA"
/db xref="taxon:10090"
/chromosome="3"
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Pred. No. 29;
1; Mismatches
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LE Herpes simplex virus VP16 vaccine Patent: JP 2002136297-A 3 14-MAY-2002; CMMENT OS 14-MAY-2001 JP 2001274-PR 02-AUG-1990 US PI RAE LYN BURKE, PC CL2N15/9, Africal Color of the color of
                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                             RESULT 4
AF021340/c
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       Human herpesvirus 2
Human herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 2818)
Terhune, S.S., Coleman, K.T., Sekulovich, R., Burke, R.L
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Herpes simplex virus VP16 vaccine.
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Spear, P.G.
                                                                                                                                             Human herpesvirus 2
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C12N15/09, A61K38/00, A61K39/245, A61P31/12, C07K14/03, C12N15/00, A61K37/02
                                                                                                                                                                                                                                                                    herpesvirus 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
938 c 886 g 40
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/db_xref="taxon:57277"
938 c 884 g
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mol_type="genomic DNA"
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95.7%;
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                         Burke, R.L.
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                                                                                                                                                             Human herpesvirus 2
Human herpesvirus 2
Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                      Human herpesvirus 2 CAM4B
U12172
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J. Infect. Dis. 178 (1), 8-15 (1998)
                                                                                                                                                                                                                                       U12172.1 GI:517447
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   Burke, R.L.
                Stuve, L.L., Brown-Shimer, S.,
                                                                                                        1 (bases 1 to 2846)
Terhune, S.S. and Spe
                                                                                                                                                                                                                                                                                          HHU12172
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                                                  Unpublished
                                                                                    Terhune, S.S. and Spear, P.G.
Variability of herpes simplex
                                                                                                                                            Alphaherpesvirinae; Simplexvirus
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                                     (bases 274 to 2846)
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LEVYTRHB1KDSGLLDYTEVQRRNQLHDLRFAD1DTV1RADANAAMFAGLCAFFBGMG
DLGRAVGKVVMGVVGGVVSAVSGVSSFMSNPFGALAVGLLVLAGLVAAFFAFRYVLQL
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LSNTLABLYVRBYMBGQDRKENATPAPLRBAPSANASVBRIKTTSSIBPARLQFTYN
HIQBHVNDMLGRIAYAWCGLQNHBLTLWNBARKLNPNAIASATVGRRVSARMLGDVA
VSTCVPVAPDNVIVQNSMRVSSRPGTCYSRPLVSFRYEDQGPLIEGQLGENNBLRLTR
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YPYDEFVLATGDFVYMSPFYGYREGSHTEHTSYAADRFKQVDGFYARDLTTKARATSP
TTRNLLTTPKFTVAWDWVPKRPAVCTWTKWQEVDEMLKAEYGGSFRFSSDAISTTFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MRGGGLICALVUGALVAAVASAAPAAPAAPAAGGVAATVAANG
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KDVTVSQWFGHRYSQPMGIFEDRAPVPPEBVIDKINAKGVCRSTAKYVRNNMETTAF
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(rootein id="AAB72100.1"
db_xref="G1:2465441"
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                                                                                                                                                           no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                          2846 bp
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glycoprotein B (UL27) gene,
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                  Pachl, C., Najarian, R., Dina, D. and
                                                                                       virus
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                                                                                       glycoproteins
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JL27) gene, complete cds.
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Structure and expression of the herpes simplex virus type 2 glycoprotein gB gene
J. Virol. 61 (2), 326-335 (1987)
87112925
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                                                           /gene="UL27"
/citation=[2]
/replace="t"
a 962 c
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/replace="g"
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/mol_type="genomic DNA"
/strain="CAM4B"
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       68.5%;
95.7%;
       Score 22.6
Pred. No.
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2.6;
90;
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                     DB 14;
                    Length 2846;
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HHU12174/c
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Submitted (11-JUL-1994) Patricia G. Spear, Microbiology-Immunology,
Northwestern University Medical School, 303 East Chicago Avenue,
Chicago, IL 60611, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structure and expression of the herpes simplex virus type 2 glycoprotein gB gene J. Virol. 61 (2), 326-335 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 2846)
Terhune,S.S. and Spear,P.G.
Variability of herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHU12174 2846 bp DNA linear VRL 05-AUG-1994 Human herpesvirus 2 MMA glycoprotein B (UL27) gene, complete cds. U12174 U12174 GI:517451
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Stuve,L.L., Brown-Shimer,S.,
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Human herpesvirus 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jnpublished
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                                                                                                                                  /translation="MRGGLICALVUGALVAAVASAAPAAPRASGUVAATVAANGGPA
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RHVNDMLGRIAVAMCELQNHEILTMAEARKLNENAIASTATVGRRYSARMLGDWAAVST
CVPVAPDNUIVQNSRVSSRFGTCYSRPLVSFRYEDQFLIEGUGENBELRITRDAL
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97
                                                                                                      RAVGKVVMGVVGGVVSAVSGVSSFMSNPFGALAVGLLVLAGLVAAFFAFRYVLQLQRN
PMKALYPLTTKELKTSDPGGVGGEGEEGAEGGGPDEAKLABAREMIRYMALVSAMERT
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36. .2741
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/mol_type="genomic DNA"
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Direct Submission Submitted (11-JUL-1994) Patricia G. Spear, Microbiology-Immunology,
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Human herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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Terhune, S. S. and Spear, P.G.
Variability of herpes simplex virus glycoproteins in clinical
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Human herpesvirus 2
Human herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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TTRALLTTKKETVAMDWVPKRPAVCTMTKWQEVDEMLRAEYGGSFRFSSDAISTTFTT
NLTESELSRVDLIGDCIGDARRAIDRWFARKYNATHIKVGQPQYYLATGGFLIAYQPL
LSWTLAELYVREYMREQDRKPENATPAPLREBAPANASYERIKTTSSIEFARLOFTYN
HIQRHVNDMLGRIAVAWCELQWHELTLWNEARKLNPNAIASATVGRRVSARMLGDVMA
VSTCVPVAPDNVIVQNSMRVSSRPGTCYSRPLVSFRYEDQGFLIEGQLGENNELRLTR
DALEFCTVGHRRYFIFGGGYVYFFEYAXSHQLSRADVTTVSTEIDLNITMLEBHBEFVP
LBVYTRHEIKDSGLLDYTEQRRNQLHDLRFADIDTVIRADANAMFAGLCAFFEGMG
DLGRAVGKVVGGVVGGVVSAVSGVSSFMSNPFCALAVGLLVLAGLVAAFFAFRYVLQL
QRNPMKALYPLTTKELKTSDEGGVGGGGGEGAEGGGFDEAKLAEAREMIRYMALVSAM
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/protein_id="AAB60546.1"
/db_xref="GI:522169"
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/mol_type="genomic DNA"
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Submitted (11-JUL-1994) Patricia G. Spear, Microbiology-Immunology, Northwestern University Medical School, 303 East Chicago Avenue,
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Terhune, S.S. and Spear, P.G.
Variability of herpes simplex virus glycoproteins in clinical
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NLTEXSLSRVDLGDCIGRDARBAIDMFARKYNATHIKVGQPQYLATGGFLIAYQPL
LSNTLAELYVREYMEQDRKPRNAIDMPAPLREBPSANAS VERIKTTSSIEFARLQFTYN
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VSTCVPVAPDNVIVQNSMRVSSRPGTCYSRPLVSFRYBDQGPLIEGQLGENNELRLTR
DALEPCTVGHRRYFIFGGGYYYFEEYAYSHQLSRADVTTVSTFIDLNITMLEDHEFVP
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NADAQPYVCPPPTGATVVQFRQPRR CPTR PEGQNYTEGIA VVPEKINI APYKFKATMYY
KDVTVSQVMFGHR YSQFMGI FEDRA PVPFEEVI DKI NAKGVCRSTAKYVRNIMETTAF
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YPYDEFVLATGDFVYMS PFYGYREGSHTEHTS YAADRFKQVDGFYARDLTTKARATS P
QRNPMKALYPLTTKELKTSDPGGVGGEGEEGAEGGGFDEAKLAEAREMIRYMALVSAM
ERTEHKARKKGTSALLSSKVTNMVLRKRNKARYSPLHNEDEAGDEDEL"
                                                                                                       LEVYTRHEI KDSGLLDYTEVQRRNQLHDLR FAD I DTVI RADANAAMFAGLCAFF BGMG
DLGRAVGKVVMGVVGGVVSAVSGVSS FMSN PFGALAVGLLVLAGLVAAFFAFR YVLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="glycoprotein B"
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/db_xref="GI:522171"
/translation="MRGGGIICALVVGALVAAVASAAPAAPAAPRASGGVAATVAANG
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REFERENCE
AUTHORS
TITLE
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Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 3324)
Bzik,D.J., Debroy,C., Fox,B.A., Pederson,N.E. and Person,S.
The nucleotide sequence of the gB glycoprotein gene of HSV-2 and comparison with the corresponding gene of HSV-1
Virology 155 (2), 322-333 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A membrane spanning region was found at position 2717-2923. The authors proposed that a signal cleavage-recognition site exits after nuclectide 613. 'This would give a mature peptide of 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HS2GB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences of gB glycoprotein genes of HSV-1 and HSV-2 were compared and there was an overall amino acid homology of 85%. There were three major regions of homology at nucleotides 108-397, 484-785, and 835-873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein; glycoprotein Human herpesvirus 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSV2 glycoprotein B gene, M14923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Draft entry and computer-readable sequence of \{1\} kindly provided by N.E.Pederson, 10-APR-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_hu_
/540
                       NLTEYSLSRVDLGDCIGRDAREAIDRMFARKYNATHIKVGQPQYYQATGGFLIAYQPL
LSNTLAELYVREYMREQDRKPRNATPAPLREAPSANASVERIKTTSSIEFARLQPTYN
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                                                                                                                                                                                                                                                                                                                                                    548. .3262
                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="vngplpdhsthspaqppntalyysvenvgllphlkeelarping
aggsgadwavsefqkfycfdgvsgitptqraawryireliiattlfasvyrcgelelr
rpdcsrptseglyryppgvyltynsdcplvaivesgfdgcigprpvvvydrdvfsily
                                                                                                                                                                                                                                                                                                                                                                                                                   SVLQHLAPRLAGGGTDAPP"
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  VATCVPVAPDNVI VQNSMRVSSRPGTCYSRPLVSFRYEDQGPLIEGQLGENNDVRLTF
                                                                                                                                                                                                                                                    /product="glycoprotein gB"
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/db_xref="GI:330255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="unknown protein"
/protein_id="AAA66439.1"
/db_xref="GI:807643"
                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                   /note="gB mRNA (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10310"
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|mol_type="genomic DNA"
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AUTHORS
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SOURCE
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ACCESSION
VERSION
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ORGANISM

Unknown

Unclassified. Unknown. I08685.1

1 (bases 1 to 3472)
Burke, R.L., Pachl, C. and Valenzuela, P.D.

3472 bp Sequence 1 from Patent WO 8802634. 108685

DNA

linear

PAT 02-DEC-1994

GI:588605

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REFERENCE
AUTHORS
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RESULT 11
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                                                                                                                                                             Local Similarity
                                                                               2349
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Vaccine for use in the therapeutic treatment of
Pateent: JP 2002167398-A 1 11-JUN-2002;
CHIRON CORP
OS Herpes simplex virus 7
PN JP 2002167398-A/1
PD 11-JUN-2002
PF 12-SEP-2001 JP 2001277340
PR 20-CCT-1986 US 921.213
PI RAB LYN BURKE, CAROL PACHL, PABLO D T VALENZI
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CC Vacci
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PR 20-OCT-1986 US 921.213
PI RAB LYN BURKE, CAROL PACHL, PABLO D T VALENZUELA PC C07K14/035, A61K39/245, A61P31/22, C12N15/09, C12N15/09, C12N15/09, PC
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Herpes simplex virus 7
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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Vaccine for use in the therapeutic
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                                                                                              CAAACTCGTGKTCCTCCAGCATG 28
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                                                                               CAAACTCGTGGTCCTCCAGCATG 2327
                                                                                                                                           68.5%;
nilarity 95.7%;
Conservative
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LEVYTRHBIKDSGLLDYTEVQRRNQLHDLRFADIDTVIRADANAMFAGLCAFFEGMG
DLGRAVGKVVAGVVGGVVSAVSAVSSEMSNPFGALAVGLLVLAGLVAAFFAFRYVQL
QRNPMKALYPLTTKELKTSDPGGVGGEGEEGAEGGFDEAKLAEAREMIRYMALVSAM
BRTEHKARKKGTSALLSSKVTNNVLRKNKARYSPLHNEDEAGDEDEL"

1063 2 2 2 1063
1161 1
                                                                                                                                                                                                                       /organism="Herpes simplex virus
/mol type="genomic DNA"
/mb xref="taxon:57277"
/db xref="taxon:57277"
I202 c 1069 g 562 t
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(309)..(3023).
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95.7%;
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; Pred. No. 89;
1; Mismatches
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Pred. No. 89;
1; Mismatches
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nt of HSV.
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           BASE COUNT
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                                                                   mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Original source text: Herpes simplex virus type 2 (strain 333) passed in Vero cells, DNA, clone pHS208.

Draft entry and computer-readable sequence for [1] kindly provided by R.C.Najarian, 28-APR-1987.

A polyadenylation signal is located at positions 3054-3059.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
         3 bp upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein gB gene
J. Virol. 61 (2), 326-335 (1987)
87112925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 3472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structure and expression of the herpes simplex virus type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stuve, L.L., Brown-Shimer, S., Pachl, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M15118.1 GI:330256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3027364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burke, R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human herpesvirus 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M15118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAACTCGTGGTCCTCCAGCATG 2327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAACTCGTGKTCCTCCAGCATG 28
                               639 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (333) glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOR USE IN THE THERAPEUTIC TREATMENT OF HSV WO 8802634-A 1 21-APR-1988;
Location/Qualifiers
                                                                                                                                                                                                                                          HRDHEITDMELKPAKVÄTRITSRGMHTTDLKYNIPSRVEÅFHRYGTTVNCI VEEVDARSV
YPYDEFVLATGDEVYNS PFYGREGSHTEHTS YAADER RYGVDEFYARDLTTKAAATSP
TTRHLTTDRETVAMIDHERRA VCTMYTKMGEVDEHLRAEYGGS FRESSDAL GTTETT
HLTDYSLSRVDLGDCI GRDAREA I DRMFARKYNATHI KVGQPQYYLATGGFLI AYQPL
ULTDYSLSRVDLGDCI GRDAREA I DRMFARKYNATHI KVGQPQYYLATGGFLI AYQPL
USNTLAELYVREYMREQDRKFBNAT PAPLIREA BSAMSVERI KTTSS I EFARLQPTYN
HI QRHVNDMLGRI AVANGELQMHELTLMWEAKKLNPNA I ASATVGRKVSARMLGDVM
HI QRHVNDMLGRI AVANGELQMHELTLMWEAKKLNPNA I ASATVGRKVSARMLGDVM
NGTCVPVAPDNVI VQNSMRVSSR PGTCYSR PLVS FRYEDQGPLI EGQLGENNELRLTR
                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAA45837.1"

/db_xref="G1:330257"

/db_xref="G2:330257"

/translation="MRGGGLICALVVGALVAAVASAAPAAPAAPRASGGVAATVAANG
/translation="MRGGGLICALVVGALVAAVASAAPAAPAAPRASGGVAATVAANG
GPASRPPPUPSPATTKAKKKKKKEPKRPERATPPDANATVAAGHATLRAHLREIKVE
NADAQPYVCPPPTGATVVQPEQPRRCPTRPEGQNYTEGIAVVFKENIAPYKFKATMYY
KDVTVSQVWFGHRYSQFMGIFEDRAPVPFEEVIDKINAKGVCRSTAKYVRNNMETTAF
/product="glycoprotein B"
1202 c 1069 g 562 t
ream of NruI site; 0.344 to 0.367 mu on HSV-2 map.
                                                                                                                                       QRNPMKALYPLTTKELKTSDPGGVGGEGEEGAEGGGFDEAKLAEAREMIRYMALVSAM
ERTEHKARKKGTSALLSSKVTNMVLRKRNKARYSPLHNEDEAGDEDEL"
                                                                                                                                                                             DALEPCTVGHRRYF1FGGGYVYFEEYAYSHQLSRADVTTVSTF1DLN1TMLEDHEFVP
LEVYTRHE1KDSGLLDYTEVQRRNQLHDLRFAD1DTV1RADANAAMFAGLCAFFEGMG
DLGRAVGKVYMGVVGGVVSAVSGVSSFMSNPFGALAVGLLVLAGLVAAFFAFRYVLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
1202 c 1069 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA
/db_xref="taxon:10310"
                                                                                            note="glycoprotein B signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="glycoprotein B precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.5%;
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Pred. No.
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n B gene,
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89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Najarian, R., Dina, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3472;
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KEYWORDS
SOURCE
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HS2GB2A/c
LOCUS
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Best Local
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                                                                                                                                                                                                                                                                  CAAT_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human herpesvirus 2
Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Original
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               simplex virus type 2 glycoprotein
/gene=
                                                                                                                                                                                                                                                                                           209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source text: Herpes simplex virus Location/Qualifiers
                                                                                                                                  /note="putative"
556. .3264
                                                                                                                                                     complement (547.
/gene="gB2"
                                                                                                                                                                                                                                                                                                    LYSVLQHLAPRLAGGGDGRPP"
                                                                                                                                                                                                                                                                                                                WARGASGADWAVSEFQKFYCFDGVSGITPTQRAAWRYIRELIIATTLFASVYRCGELE
LRRPDCSRPTSASLYRYPPACDLTYNSDCPLVAIVESGPDGCIGPRSVVVYDRDVFSI
                                                                          /product="glycoprotein B"
/protein_id="AAA60540.1"
/db_xref="GI:623400"
                                                                                                                                                                                   /gene="gB2"
                                                                                                                                                                                                                                                                                                                                               /codon_start=3
/product="unknown protein"
/protein_id="AAA60539.1"
/db_xref="GI:623399"
                                                                                                                                                                            note="putative"
                                                                                                                                                                                                            note="putative"
                                                                                                                                                                                                                         gene="gB2"
                                                                                                                                                                                                                                               note="putative"
                                                                                                                                                                                                                                                         'gene="gB2"
                                                                                                                                                                                                                                                                                                                                                                                                      map="0.345-0.370"
                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:10310"
                                                                                                                                                                                                                                                                                                                                                                                                                          strain="333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:341245
                                                                                                             codon_start=1
                                                                                                                        gene="gB2"
                                                                                                                                                                                                                                                                                                                                      translation="SSSTGPCSTTPPTASPSPPTPRCTTASRTWGSCRTSRRNSPASS
                                                                                                                                                                                                                                                                                                                                                                                             .548
                                                                                                                                                                                                                                                                                                                                                                                                                                        _type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22.6;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                   .556)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B (gB2) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (strain 333) DNA
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REFERENCE / AUTHORS
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AUTHORS
TITLE
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HSV2HG52
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
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ORIGIN
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  major capaid protein; membrane-associated phosphoprotein; minor capaid protein; membrane-associated phosphoprotein; minor capaid protein; neurovirulence factor; protease; protein kinase; ribonucleotide reductase large subunit; ribonucleotide reductase small subunit; RL1 gene; RL2 gene; RS1 gene; tegument protein; thymidine kinase; UL15 gene; UL10 gene; UL11 gene; UL12 gene; UL13 gene; UL18 gene; UL19 gene; UL19 gene; UL19 gene; UL19 gene; UL20 gene; UL20 gene; UL10 gene; UL10 gene; UL10 gene; UL10 gene; UL20 gene; UL30 gene; UL40 gene; UL50 gene; UL40 gene; UL50 gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Φ
    2 (bases 1 to 154746)
Everett, R.D. and Fenwick, M.L.
                                                                                                                                                                                                                                            McGeoch, D.J., Moss, H.W., McNab, D. and Frame, M.C.
DNA sequence and genetic content of the HindIII 1 region
short unique component of the herpes simplex virus type 2
identification of the gene encoding glycoprotein G, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z86099.2 GI:6572414 capsid associated tegument
                                                                                                                                                                                                          evolutionary comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human herpesvirus 2
Human herpesvirus 2
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                                                                                                                                                                                                                                                                                                                                                                                                                    Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 154746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae
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                                                                                                                                                                   Virol. 68 (Pt 1), 19-38 (1987)
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/note="putative"
622. .3261
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NPMKALYPLTTKELKTSDPGGVGGEGEEGAEGGGFDEAKLAEAREMIRYMALVSAMER
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TCVPVAPDNV I VQNSMRVSSRPGTCYSRPLVSFRYEDQGPLMEGQLGENNELRLTRDA
LBPCTVGHRRYP I PGGGYVYFEEYAYSHQLSRADVTTVRTF I DLN I TMLEDHEFVPLE
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NTLAELYVRBYMRBQDRKPRNATPAPLRBRPSANASVERIKTTSSIBFARLQFTYNHI
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3295. .3300
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; Pred. No. 89;
1; Mismatches
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McGeoch, D.J., Cunningham, C., McIntyre, G. and Dolan, A.
Comparative sequence analysis of the long repeat regions a
adjoining parts of the long unique regions in the genomes
simplex viruses types 1 and 2
J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
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On Dec 13, 1999 this sequence version replaced Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (25-FRB-1997) A. Dolan,
Street, Glasgow,, G11 5JR, UK
revised bu [6]
6 (bases 1 to 154746)
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Barnett, B.C., Dolan, A., Telford, E.A., Davison, A.J. and McGeoch, D.J. A novel herpes simplex virus gene (UL49A) encodes a putative membrane protein with counterparts in other herpesviruses J. Gen. Virol. 73 (Pt 8), 2167-2171 (1992)
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/number=2
1738. .1743
2303. .5368
/gene="RL2"
join(2303. .
                                                                                                                                                                         /rpt_family="5"
                                                                                                                                                                                                                            /rpt_family="6"
943. .1070
                                                                                                                                                                                                                                                                          /rpt_family="7"
461. .547
                                                                                                                                                                                                                                                                                                                                                                                                        440.
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/mol_type="genomic DNA"
|strain="HG52"
/db_xref="taxon:10310"
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Vpaydsgtavesapaassllrrwllvpqaddsdapayprpgapaybapayprbapaybasppsegggrap
eaphhaapaacepppprkergprpliphialrrtteylarlslrrrppasppad
aprgkvcfsprvqvrhlvawetaarlarrgswareradrdrrrrrvaaaeavigpcle
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/gene="RL1"
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/protein_id="CAB06759.1"
/db_xref="GI:1869821"
/db_xref="SWISS-pROT:P28283"
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                                                                                                                        product="neurovirulence factor
                                                                                                                                                                                                                                                                                                                                                                            gene="RL1"
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     .2377,2785. .3462,3644. .5368)
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                                                                                                                                                                                                                                                                                                                                                                                                                       /Godon_start=1
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/db_xref="Gl:1869923"
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FLEDLSHSVFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRC
VGRRDLRPANTTSTWEFPVSSDDEASSQSKPLATQPPVLALSNAPPRRVSPTRGRRRH
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9276. .9297
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/gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \translation="MEPRPGTSSRADPGPERPPROTPGTOPAAPHAWGMLADMOWLAS SDSEEETEVGISDDILARDSTSRAGSTTTEMFERGLMDAATPPARPARENGSFTPAR AQGSCGGGPVGEEEAEAGGGDVGAVCTDEIA BPLRCOSFFCLHPFCIFCMKYWIPLA MTCPLCNTPVAXLIVGVTASGSFTIPIVNDPRTRVEAEAAVRAGTAVDFIWTGNPRT APRSLSIGGHTVRALSFTPWPCTDDEDDDLADVDYVPPAPREAPRRGGGGAGATRGT SQPAATRAFPGAGRASSGGAPLAGTAGGTSAGATRAGTSGGAATRGTSTAGATRAGTSAGATRAGTSGGAATRGTSAGATRAGTSGGAATRGTSAGATRAGTSGGAATRGTSAGATRAGTSGGAATRGTSAGATRAGTSGGAATRGTSAGATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGAATRAGTSGGAATRAGTSGGAATRAGTSGGAATRAGTSGAATRAGTSGGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAGTSGAATRAG
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associated transcripts (LAT's)"
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/codon_start=1
/product="uracil-DNA glycosylase"
/protein_id="CAB06762.1"
/db_xref="GI:1869824"
/db_xref="SWISS-PROT:P28275"
/translation="MFSASTTPEQPLGLSGDATPPLPTSVPLDWAAFRRAFLIDDAWR
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/codon_start=1
/protein_id="CAB06760.1"
/db_xref="GI:1869822"
                                                                                                                                                                                                                                                                                 'gene="UL2"
|0211. .10978
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AT species)"
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|644. .5368
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                                                                                                                                                                                                                                                 'gene="UL2"
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gene="UL1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family="3"
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MEDLINE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-AUG-1999) Molecular Neuro-Oncology Laboratory, Massachusetts General Hospital, 149, 13th Street, Charlestown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 2281)
Pohl,U., Smith,J.S., Tachibana,I.,
Jenkins,R.B. and Louis,D.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2281)
Pohl,U., Smith,J.S., Tachibana,I., Ueki,K., Lee,H.K., Ramaswamy,S. Wu,Q., Mohrenweiser,H.W., Jenkins,R.B. and Louis,D.N.
EHD2, EHD3, and EHD4 encode novel members of a highly conserved family of EH domain-containing proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 CABACTCGTGKTCCTCCAGCATG 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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/gene="UL3"
11033. .11734
/gene="UL3"
/product="EH domain containing 3"
/protein id="AAP40471.1"
/db_xref="GI:7212809"
/tanalation="WF2809"
/tranalation="WF2809"
/tranala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLLEPELANPLTARLLABYDRRCQTEEVLPPREDVFSWTRYCTPDDVRVVIIGQDPYH
HPGQAHGLAFSVRADVFVPPSLRNVLAAVKNCYPDARMSGRGCLEKWARDGVLLLNTT
LTVKRGAAASHSKLGWDRFVGGVVQRLAARRPGLVFMLWGAHAQNAIRPDPRQHYVLK
FSHPSPLSKYPFGTCQHFLAANRYLETRDIWFIDWSV"
                                                                                                                                                                                                                                                                                                                                     /note="similar to EHD1; contains ATP/GTP binding motif;
bipartite nuclear localization signal; EP-hand motif"
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11033. .11734
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="EHD3"
45. .1685
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/protein_id="CAB06763.1"
/db_xref="GI:1869825"
                                                                                                                                                                                                                                                                                                                                                                                                   /gene="EHD3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:9606"
chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        map="2p21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="brain"
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95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stage="fetus"
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Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ueki, K., Lee, H.K.,
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| Search completed: September 16, 2003, 19:14:19 Job time : 724.713 secs | Oy 4 TGCAAACTCGTGKTCCTCCAGCATGC 29 | Query Match 67.9%; Score 22.4; DB 9; Length 2281; Best Local Similarity 88.5%; Pred. No. 1.1e+02; Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0; | LAEIYGRIEREHQISPGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVDDMLAHDIAQ LMVLVRQBESQRFIQMVKGGAFEGTLKGPGRGYGEGAGEGIDDAEWVVARDKEMYDE IFYTLSPVDGKITGANAKKEMVRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLI KVKLEGHELPNELPAHLLPREGKLPSDGVGGHSDGQC" BASE COUNT 541 a 639 c 653 g 448 t ORIGIN |
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Sequence encoding
N. meningitidis pa
Neisseria meningit
N. meningitidis B
DNA encoding novel

Sequence of Herpes DNA fragment encod

Glycoprotein B (gB Herpes simplex vir

Herpes simplex vir Recombinant herpes HSVgB gene. Herp

Truncated HSVgB ge Herpes Simplex Vir HSV surface antige

Human polynucleoti N. gonorrhoeae nuc Human polynucleoti cDNA of human EHD2

Human herpesvirus

Human nervous syst
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Breast carcinoma

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HSV-2 strain SB5 C
Herpes Simplex Vir
Sequence encoding
HSV-2 strain SB5 C
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04-NOV-1996;
                                                                                           31-OCT-1997;
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                                                                                                                                                                                                                                                                                       HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                      AAV62158;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV62158 standard; DNA; 2645 BP.
                                                                                                                         14-MAY-1998.
                                                                                                                                                      WO9820016-A1
                                                                                                                                                                                                                                                                                                                                    HSV-2 strain SB5 Contig ID 14 DNA sequence.
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ABV94417
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Database

Sequence:

8

Regult No.

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RESULT 2
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Vaccin
KW Vaccin
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Herpes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chan JY,
Esser KM,
                                                                                                                                                                                                                                                                                                                                                 vaccine; prophylaxiв;
glycoprotein; gB; вв.
                                                                                          Amino acid chain of glyco:protein recombinant and used for vaccines
                                                                                                                                 WPI; 1987-056354/08
P-PSDB; AAP71136.
                                                                                                                                                                                                                          20-JUN-1984;
                                                                                                                                                                                                                                                   20-JUN-1984;
                                                                                                                                                                                                                                                                             10-FEB-1987.
                                                                                                                                                                                                                                                                                                      US4642333-A.
                                                                                                                                                                                                                                                                                                                             Herpes simplex virus type 2
                                                                                                                                                                                                                                                                                                                                                                                           Herpes Simplex Virus-2 gB from p52BXX.
                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
30-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN71399 standard; DNA; 2724 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes simplex virus type-2 sequences - and treatment of infection or inducing i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-286847/25.
              'N' indicated nucleotide to be determined (corresp. 17.41 of HSV-1 gB)
                                                     Example;
 pure non-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     755
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                                                    Table 2; 16pp; English
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Leary JJ;
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(first entry)
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95.7%;
                                                                                                                                                                                                                                                                                                                                                                   treatment;
  amino acid
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; Pred. No. 17;
1; Mismatches
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for herpes
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 chain comprising a sequence
                                                                                                                                                                                                                                                                                                                                                                    Simplex Virus-1;
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simplex
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                            to residues
                                                                                       prepd. as
virus types 1
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ID AANSO15
XX AANSO15
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DE Sequen
DE Cype 2
XX Vaccin
XX PT CDS
FT CDS
CC TTGD
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(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                    sequence corresponding to that occurring in glycoprotein B of HSV-or HSV-2. Preferably, when the chain comprises a sequence corresp. to that occurring in glycoprotein B of HSV-2, it contains 4-750 AA residues. The chain esp.has a molecular wt. of 65000 daltons and
                                                                                                                                                   The inventors claim a non-glycosylated amino acid chain comprising sequence corresponding to that occurring in glycoprotein B of HSV-1
                                                            Sequence
                                                                                                                                                                                                 Disclosure; Table 2, Page 35-35C; 40pp; English.
                                                                                                                                                                                                                              New amino acid chains of glyco-protein B of herpes simplex virus - prepd. by recombination DNA methods for use in vaccines
                                                                                                                                                                                                                                                                            WPI; 1985-039636/07.
                                                                                                                                                                                                                                                                                                          Person
                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1983;
23-JUN-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP133063-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding the glycoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAN50517;
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                                                                                        includes AA residues 165-629 from the HSV-2 glycoprotein
                                                                                                                                                                                                                                                                                                                                       (PERS/) PERSON
                                                                                                                                                                                                                                                                                                                                                                       20-JUN-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (HSV-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 95.7
22; Conservative
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAPACTCGTGGTCCTCCAGCATG 2028
                                                             2727
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
                                                            BP; 493 A; 913 C; 855 G;
                                                                                                                                                                                                                                                                                                                                                                   83US-0532996.
83US-0506986.
84US-0622496.
                                                                                                                                                                                                                                                                                                                                                                                                                                 84EP-0401312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 A; 911
            68.5%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.5%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2727
٠,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22.6;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
              Score 22.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           854
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (gB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 T;
                                                            391 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Herpes simplex virus
                              ٠.
د
                                                             75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
 ..
                            Length 2727;
                                                             other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                          B sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 G
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSV-2
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CAAACTCGTGKTCCTCCAGCATG 28

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RESULT 4
AAV621146/c
ID AAV6211
XX AAV621
XX AAV621
XX HSV-2
XX HSV-2
XX HSV-2
XX HCPP88
XX HCPP
RESULT '5
AAT93650/c
ID AAT936
XX
AC AAT936
XX
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain SB5 (deposited as ATCC VR-2546), is designated Contig ID 91, and encodes a HSV-2 protein. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Altagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-1997;
04-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1998
                             AAT93650;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2841 BP; 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 284-285; 748pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chan JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9820016-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes simplex virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSV-2 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV62146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV62146 standard; DNA;
                                                                              AAT93650 standard; DNA; 3471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-286847/25.
DB; AAW72062.
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                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                Similarity
22; Conserv
                                                                                                                                                                                                             CAAACTCGTGGTCCTCCAGCATG 2049
                                                                                                                                                                                                                                          CAAACTCGTGKTCCTCCAGCATG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAACTCGTGGTCCTCCAGCATG 2031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dabrowski-Amaral CE,
Leary JJ;
                                                                                                                                                                                                                                                                                                                68.5%;
llarity 95.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SB5 Contig ID 91 DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0049018.
96US-0030279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                    A; 921 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2841
                                                                                                                                                                                                                                                                                                              Score 22.6; D
Pred. No. 18;
1; Mismatches
                                                                                                                                                                                                                                                                                                                1;
                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delvecchio
                                                                                                                                                                                                                                                                                                                                                                                                                       915 G;
                                                                                                                                                                                                                                                                                                                                                                                                                       425 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon
                                                                                                                                                                                                                                                                                                                                                              Length 2841;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                Gaps
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PX8XWWWX8XHFFFFFFFFFFFFFFFFFX9X8XRRRRXXQXFXRRXFFX8XX333333333
 밁
                     8
                                                 Matches
                                                            Query Match
Best Local Similarity
                                                                                                                    The present sequence is from the Herpes simplex virus (HSV) type I strain Patton and encodes a glycoprotein B. HSV is a double strained virus packaged within an icosohedral inucleocapsid enveloped within a membrane. The membrane includes a number of virus-specific glycoproteins, with glycoprotein B being one of the most abundant. Glycoprotein B from both HSV type I and type II are cross reactive. New vaccines comprising recombinantly produced glycosylated glycoprotein B that has a deletion of at least part of the transmembrane anchor region, in combination with a carrier and an adjuvant have been produced. The vaccines are used for immunising humans against HSV (HSV type 1) by vaccination before or after primary infection with HSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus; HSV; type I; type II; glycoprotein membrane protein; virus-specific glycoprotein; transmembrane anchor region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herpes simplex virus type 1.
                                                                                                                                                                                                                                                                                               Vaccines against herpes simplex virus infection - containing recombinant HSV glycoprotein B
                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-372022/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-1986;
06-APR-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1998 (first entry)
                                                                                                Sequence
                                                                                                                                                                                                                                                                        Disclosure; Fig 4A-F; 33pp; English
                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW34552.
                                                                                                                                                                                                                                                                                                                                                                         Burke RL, Pachl C,
                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-1990;
21-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5648079-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAT_signal
                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR )
 2349
                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     simplex virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                   CHIRON
                                                                                                3471
CAMACTCGTGGTCCTCCAGCATG 2327
            CAMACTCGTGKTCCTCCAGCATG 28
                                                 Conservative
                                                                                                BP; 639 A; 1201 C; 1069 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                    86US-0921730.
84US-0597784.
90US-0587179.
92US-0993415.
                                                                                                                                                                                                                                                                                                                                                                                                   CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0138717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0351875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3409..3416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3166..3173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "putative"
309..3023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= d
/note= "putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                            Valenzuela
                                                           68.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycoprotein B
                                                 1;
                                                            Score 22.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                            PDT;
                                                  Mismatches
                                                            18;
                                                                                                562 T; 0 other;
                                                                        DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding
                                               0;
                                                                        Length
                                                  Indels
                                                                         3471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B; vaccine;
                                               <u>.</u>
                                               Gaps
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RESULT 6
AAN80907/c
ID AAN80907 standard; DNA; 3472
                                                                                                                                        AAQ48496/c
ID AAQ48496
                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                            Prepn. of recombinant gB and gD is described in W088504587. The amino acid sequence and DNA sequence for gB 1 presented in AAP80914 and AAN80907 differ from that originally presented in Table 1 of International Publication No. WO 85/04587. The DNA sequence in Table 1 contains an error in that an additional nucleotide (G) is listed at position 607 which resulted in a shift in reading frame relative to AAN80907 from which this nucleotide has been deleted.
Glycoprotein; gB1; gB2; herpes simplex virus; HSV-1; HSV-2; flanking; initiation; termination; transcription; translation;
                                         Glycoprotein B (gB1).
                                                                    25-MAR-2003
29-MAR-1994
                                                                                                             AAQ48496;
                                                                                                                                                                                                                                                                                                                     Sequence 3472 BP; 639 A; 1202 C; 1068 G; 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine for treatment of herpes simplex virus - recombinant HSV glyco:proteins B and D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1988-119368/17.
P-PSDB; AAP80914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burke LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1987;
20-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO8802634-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; herpes simplex virus; therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of Herpes simplex virus (HSV) glycoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
09-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAN80907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                 (Updated
                                                                                                                                                                                                             2349
                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                        თ
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                          CAAACTCGTGKTCCTCCAGCATG
                                                                                                                                        standard;
                                                                                                                                                                                                             CARACTOGTGGTCCTCCAGCATG 2327
                                                                                                                                                                                                                                                                                                                                                  on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 4; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pachl C,
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
(first ent
                                                                   (updated)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87US-0079605.
86US-0921213.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
309..3023
                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                    entry)
                                                                                                                                                                                                                                                                            68.5%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Valenzuela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                        3472
                                                                                                                                                                                                                                                                ۲.
                                                                                                                                                                                                                                                                             Score 22.6;
Pred. No. 16
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                            9,
                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contains
                                                                                                                                                                                                                                                                                          Length 3472;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (gB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \vdash
                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                  0
밁
                                                                                                                                                                                                                                                                                                                                                                          ફ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 22
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20-OCT-1986;
20-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA constructs for expressing a glycosylated polypeptide in a eukaryotic host cell comprises (1) an oligonucleotide sequence (OS) free of natural flanking sequences, encoding glycoprotein B (gB) of HSV, or its fragments, and (2) 5' initiating and 3' terminating transcriptional and translational regulatory sequences flanking OS, at least one of these sequences not being from HSV. The HSV-1 and HSV-2 sequences are given in AAQ48496 and AAQ48497 respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burke RL,
                                                                                                                         Herpes simplex virus type
                                                                                                                                                     HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
                                                                                                                                                                                                                          13-JAN-1999
                                                                                                                                                                                                                                                   AAV62176;
                                                                                                                                                                                                                                                                             AAV62176 standard; DNA; 117213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA construct for expressing HSV glycosylated polypeptide useful for vaccinating against HSV-1 and -2 infections
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22; Conserv
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                                                                                                                                                                                             SBS Contig ID 15 DNA sequence
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86US-0921730.
90US-0587179.
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                           /product= "ORF#1 protein"
/note= "encoded protein s
1170..2174
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 /product=
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755..1297
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95.7%;
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 "ORF#2 protein"
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Pred. No. 18;
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| | = "ORF#27 protein" 'encoded protein shown in AAW7219 ent (4485347297) ak | <pre>/note= "encoded protein shown in AAW72191" 42206.44178 /*tag= aj /trans1 except= (pos: 4406344064, aa: Lys)</pre> | ncoded 973 | /note= "encoded protein shown in AAW72189" 390903935 /*tag= ah /product= "ORF#25 protein" | ct= "ORF# "encoded ment (380 ag | 로 : 2 | 22a protein" protein shown in | ment (3206732735) ac ct= "ORF#21 protein" "encoded protein shown in AAW7218 | ment (2763031784) ab ct= "ORF#20a protein" "approded protein shown in AAW? | <pre>nent (2763031754) aa abctrick protein" st= "ORF#20b protein" "encoded protein shown in AAW7222</pre> | ment (2629527251) ct= "ORF#19 protein" rencoded protein shown in AAW7218 | .25955 Y "ORF#18 protein" "encoded protein shown in Alw72185 | ncoded pr t (22546. "ORF#17 | HOWIT THE MANY/210 | protein shown in ANN 2102 | <pre>complement (1941520074) /*tag= u /product= "ORF#14 protein" /note= "encoded protein shown in AAW72181"</pre> | <pre>/*tag= t /product= "ORF#13 protein" /note= "encoded protein shown in AAW72180"</pre> |

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RESULT 9
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Best Local Similarity
Matches 22; Conserv
        Orson
                                                                                                              Human herpesvirus
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                                                                                                                                                                                 Human herpesvirus 2 complete
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                                                          06-APR-2001; 2001WO-US11372
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                         (BAYU ) BAYLOR COLLEGE MEDICINE
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        Kinsey BM,
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/note= "encoded pr
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/note= "encoded protein shown
complement (47305..49662)
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Pred. No. 29;
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disease;
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                                  CC bound to an aggregated protein-polycationic polymer conjugate or CC suspension. The expression vector contains a promoter polymucleotide C sequence operatively linked to a polymucleotide sequence encoding an CC antigen which is a fragment of a gene or genome associated with an CC infectious disease, cancer and autoimmune disease such as rheumatoid CC arthritis, vasculitis, and multiple sclerosis, pathogenic genomes CC consisting of bacterium, fungus, protozoa and virus such as human CC immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis C C virus (HCV), influenza and respiratory syncytial virus (RSV), and CC virus (HCV), influenza and respiratory syncytial virus (RSV), and CC contains expression vector), is useful for inducing an immune response (systemic and/or mucosal) in an organism. The cytokine expression vector CC (GM-CSP) or interleukin-12 (IL-12). The polymucleotide sequences encoding the antigen and the cytokine are under transcriptional control of same or CC different promoter polymucleotide sequences. The expression vector, as a CC DNA vaccine is useful for treating a condition in an organism. The CC other invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for oral delivery of vaccines, comprises expression containing antigenic genomic sequence, bound to aggregated protein-polycationic polymer conjugate or suspension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 90-132; 145pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               co a composition comprising an expression protein-polycationic polymer conjugate or
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                                   Matches
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Best Local
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                                  Similarity
22; Conser
CAAACTCGTGGTCCTCCAGCATG 54099
                 CAAACTCGTGKTCCTCCAGCATG 28
                                   Conservative
                                          68.5%;
95.7%;
                                  1; Mismatches
                                           Score 22.6;
Pred. No. 30;
                                                    DB
                                                     24;
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                                                   Length 154746;
                                   Indels
                                   0
                                   Gape
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Sequence 154746 BP;

23003 A;

54218 C; 54701

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22824 T;

0 other;

0

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Human polynucleotide SEQ ID
                              22-OCT-2001 (first entry)
                                                                                                 AAI61247
                                                                                                 standard; cDNA; 2550
                                                                                                 ВP
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NO 5236

AAI61247/C
ID AAI61
XX AAI61
XX AAI61
XX AAI61
XX AAI61
XX Human
XX Human
XX Human
XX Homo
KW Alzhe
KW Alzhe
KW Chemc
KW Ieuka
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's parkinson's disease; huntington's disease; hambington's disease; hambington's disease; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotinetic; thrombolytic; drug screening; arthritis; inflammation; lentrammation; 09-JUL-2000; 19-JUL-2000; 21-JAN-2000; 25-APR-2000; 26-DEC-2000; WO200153312-A1 Homo sapiens. 26-JUL-2001. leukaemia; 88. 2000WO-US34263 2000US-0598042. 2000US-0488725 cancer;

14-SEP-2000; 19-OCT-2000; 03-AUG-2000;

2000US-0662191 2000US-0693036 2000US-0620312

2000US-0653450.

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RESULT 11
AAL53531/c
ID AAL53531 standard; cDNA; 2815 BP
XX
AC AAL53531;
XX
DT 30-JAN-2003 (first entry)
XX
CDNA of human EHD2 gene, SEQ ID
XX
CYtostatic; osteopathic; recombi
KW Cytostatic; osteopathic; recombi
KW EHD2; endocytosis; IGF1 signalin
KW metastasis; bone formation; oste
XX
FH Key I Location/Qualifi
FT CDS 1.1001
FT CDS /*tag= a
FT XX
PN US2002115069-A1.
XX
PD 22-AUG-2002.
XX
PF 17-MAY-1999; 99US-0312762.
XX
PR 21-FEB-1997; 97IL-0120283.
PR 21-FEB-1998; 98US-0026898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The invention relates to human nucleic acids (AAI57798-AAI61369) and Ct the encoded polypeptides (AAM38642-AAM42213) with nootroppic, immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide CC of the invention may be used to treat diseases of the peripheral nervous System, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC Altheimer's, Parkinson's disease, Huntington's diseases, such as CC lateral Sclerosis, and Sy-Drager Syndrome. Other uses include the CC utilisation of the activities such as: Immune system suppression, CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, arthritis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed CC enceptication.
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Best Local
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Zhao
                                                                                                                                                                                                                                                                             Cytostatic; osteopathic; recombinant Eps15 homology; EH domain; EHD2; endocytosis; IGF1 signaling; suppressing adhesion; invasion
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DB; AAM42091.
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Wang Z
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Wehrman T, X
Goodrich R,
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Pred. No. 2:
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Zhang J;
                                                                                                                                                                                                                                                                                invasion
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21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel recombinant Eps15 homology (EH) domain containing protein 1 or 2 (EHD1 or EHD2) with an N-terminal region containing a nucleotide binding consensus site, a central coiled coil structure and a C-terminal region including an EH domain, where the polypeptide participates in endocytosis. The peptides, peptide analogues and/or the polynucleotide sequences are useful for regulating EHD1/2 protein activity in vivo, where the EHD1/2 protein and its gene are useful for upregulating the protein activity. The novel method is useful for lowering the rate of IGF1 signaling and therefore useful for suppressing adhesion, invasion and metastasis where EHD is overexpressed, and therefore endocytosis. The method is also useful for elongating IGF1 effects and therefore for increasing bone formation in osteoporosis conditions. This polynucleotide sequence represents the cDNA of a human EHD2 gene of the invention.
                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant Eps15 homology domain containing protein useful for regulating endogenous EHD protein by regulating insulin-like growth factor 1 receptor cell signaling via altered clathrin coated pit mediated endocytosis -
                                                                                                                      26-DEC-2000;
                                                                                                                                                      26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI59461 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2815 BP; 695 A; 754 C; 730 G; 636 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horowitz M,
                                                                                                                                                                                                                                               leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HORO/) HOROWITZ M.
(MINT/) MINTZ L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                               sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Page 45-46; 88pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 TGCAAACTCGTGKTCCTCCAGCATGC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGCAAACTCGTCGTCGTCCAGCATGC 955
                                            2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
               2000US-0653450.
2000US-0662191.
                                                                                                                       2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA; 3327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1:
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Pred. No. 2:
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RESULT 13
ABZ41610/c
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         WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disnovers
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Wang
Zhao
                                                                                                                                                    WO200279243-A2
                                                                                                                                                                          Neisseria
                                                                                                                                                                                             Antibacterial; infection; vaccine; gene therapy; gene; ds
                                                                                                                                                                                                                    z.
                                                                                                                                                                                                                                          07-MAR-2003
                                                                                                                                                                                                                                                              ABZ41610;
                                                                                                                                                                                                                                                                                     ABZ41610
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3327
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and such as central nervous
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                                         Fontana
                                                                                   12-FEB-2001; 2001GB-0003424
                                                                                                                               10-OCT-2002
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                                                                                                         12-FEB-2002; 2002WO-IB02069
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                                                              (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                   gonorrhoeae
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DB; AAM40305.
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                    2003-058415/05
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          ABP80640
                                                             CHIRON
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                              TGCAAACTCGTGKTCCTCCAGCATGC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1664; 10078pp; English.
                                                                                                                                                                        gonorrhoeae.
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                       Pizza M,
                                                                                                                                                                                                                                        (first entry)
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                                                             SPA.
                                                                                                                                                                                                                  nucleotide sequence
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Wehrman T,
                                                                                                                                                                                                                                                                                    DNA; 1494
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                                                                                                                                                                                                                                                                                                                                                                                            67.9%;
88.5%;
                                       Maeignani V,
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                                                                                                                                                                                                                                                                                    ВÞ
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Pred. No. 22
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Xue
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                               other;
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Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                         3327;
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RESULT 14
AAQ14479/c
ID AAQ14
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Matches
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                   The sequence encodes a truncated form of the HSVgB polypeptide. The recombinant protein can be used to prepare vaccines for prophylaxis of HSV infection and for use in diagnostic kits. See also AAQ14478.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                       30-NOV-1989;
22-JUN-1989;
21-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins are antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention.
                                                                                                               HSVgB polypeptide(s) obtd. useful as vaccines against cheaply and safely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection \,\,
                                                                                         Claim 3; Fig 7; 24pp; Japanese
                                                                                                                                                                                                                                                                                             25-SEP-1991.
                                                                                                                                                                                                                                                                                                                    JP03218397-A.
                                                                                                                                                                                                                                                                                                                                                                                       Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
23-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ14479;
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                                                                                                                                                               P-PSDB;
                                                                                                                                                                            WPI; 1991-328397/45
                                                                                                                                                                                                                                                                      21-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Truncated HSVgB gene.
                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD
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25; Conser
                                                                                                                                                               AAR14666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                       89JP-0308941.
89JP-0158238.
90JP-0161448.
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                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.8%;
75.8%;
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Pred. No. 5
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                                                                                                                           recombinant DNA techniques V and in diagnosis, can be p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Sequence

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620 G;

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other;

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RESULT 15
AAN71303/c
ID AAN71303 standard; DNA; 2712 BP.

XX
AC AAN71303;
XX
AC AAN71303;
XX
DT 25-MAR-2003 (updated)
DT 30-APR-1991 (first entry)
XX
DE Herpes Simplex Virus-1 gB from pKB;
XX
Vaccine; prophylaxis; treatment; H;
XX
US4642333-A.
XX
OS Herpes simplex virus type 1 (KOS).
XX
VIOLET 1987.
XX
VIOLET 1987.
XX
PN US4642333-A.
XX
PN PPSDB; AAP71135.
XX
PN WPI; 1987-056354/08.
XX
PN WPI; 1987-056354/
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Search completed: September 16, 2003, 18:37:07 Job time : 167.327 secs
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                                                                                                                                                                                                                                                                Query Match 64.8%; Score 21.4; DB 8; Best Local Similarity 95.7%; Pred. No. 54; Matches 22; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 22; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A pure non-glycosylated amino acid (AA) chain comprising a sequence corresponding to that occurring in glycoprotein B of HSV-1 or HSV-2 virus which is antigenic to HSV-1 of HSV-2, which contains no more than 750 AA residues, and which includes AA residues 135-649 inclusive is claimed. It can be used to produce vaccines for prophylaxis and treatment of HSV-1 and HSV-2. See AAN/1399 for the HSV-2 sequence. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2712 BP; 519 A; 945 C; 849 G; 397 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid chain of glyco:protein B of HSV-1 and 2 - prepd. as recombinant and used for vaccines for herpes simplex virus types 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus type 1 (KOS).
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                                                                                                                                                                          CAAACTCGTGKTCCTCCAGCATG 28
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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1: /cgm2_6/ptodata/2
2: /cgm2_6/ptodata/2
3: /cgm2_6/ptodata/2
4: /cgm2_6/ptodata/2
5: /cgm2_6/ptodata/2
6: /cgm2_6/ptodata/2
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Match
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Maximum Match 100%
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Copyright (c) 1993 - 2003 Compus
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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US-09-149-727-7
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US-09-149-727-7
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US-09-09-159-452A-1
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US-09-312-762A-2
US-09-312-762A-6
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US-07-906-930E-3
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Sequence 7, Appli
Sequence 13, Appl
Sequence 13, Appl
Patent No. 5244792
           Sequence 1, Appli
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Sequence 2, Appli
Sequence 358, App
Sequence 359, App
Sequence 27, Appli
Sequence 7, Appli
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| 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.6 | 17.6 | 17.6 | 17.6 | 17.6 | 17.6 | 17.6 | 17.8 | 17.8 | 17.8 | 17.8 | 18 |
| 52.7 | 52.7 | 52.7 | 52.7 | 52.7 | 52.7 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.3 | 53.9 | 53.9 | 53.9 | 53.9 | 54.5 |
| 1340 | 1340 | 1340 | 1340 | 1098 | 576 | 8802 | 8802 | 4167 | 1623 | 1122 | 795 | 624 | 5084 | 5084 | 3627 | 2311 | 1112 |
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| Sequence 4, Appli | , , | Sequence 4, Appli | Sequence 2, Appli | Sequence 13595, A | Sequence 13853, A | Sequence 1, Appli | Sequence 1, Appli | Sequence 3666, Ap | Sequence 3844, Ap | Sequence 1, Appli | Sequence 3803, Ap | Sequence 43, Appl | Sequence 25, Appl | Sequence 21, Appl | Sequence 1, Appli | Sequence 26, Appl | Sequence 136, App |

ALIGNMENTS

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APPLICANT: BURKE, RAE L.;1
TITLE OF INVENTION: EXPRES;
B FROM HERPES SIMPLEX VIRUS;
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09312762A Patent No. 6552177
GENERAL INFORMATION:
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FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 921,730
FILING DATE: 20-OCT-1986
APPLICATION NUMBER: 597,784
PRILING DATE: 06-APR-1984
                                                                                                                                                                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 me;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MIA HOROWITZ ET AL.
TITLE OF INVENTION: EH DOMAIN CONTAINING GENES AND PROTEINS NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
COMPUTER: Twinhead* SILMADON OF CONTROL OF C
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CITY: Arlington
STATE: Virginia
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Twinhead* Slimnote-890TX
                                                                 for Windows version 2.0
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N: EXPRESSION
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                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,439A
PILING DATE: Pebruary 21, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 39,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application Patent No. 6015565
GENERAL INFORMATION:
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Best Local Similarity
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REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 916/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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LENGTH: 2815
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APPLICATION NUMBER: 09/02
FILING DATE: 20 FEB 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rose, Timothy M. APPLICANT: Bosch, Marnix L. APPLICANT: Strand, Kurt
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STRANDEDNESS: double
                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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STREET: 4225 Executive Square, Ste 1400
                                                           ENGTH: 2713 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           980 TGCAAACTCGTCGTCGAGCATGC 955
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                                                                                                                                                       (619) 678-5099
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOPROTEIN B OF THE RFHV/KSHV
SUBFAMILY OF HERPES VIRUSES
113
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Pred. No. 1
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5244792-2/c

;PATENT NO. 5244792

; APPLICANT: BURKE, RAE L.;PACHL, CAROL;V
; APPLICANT: BURKES, RAE L.;PACHL, CAROL;V
; APPLICANTION: EXPRESSION OF RECOM
; FROM HERPES SIMPLEX VIRUS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-720-229-13/c
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ZIP: 94304-1018

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,229
FILING DATE: 26-SEP-1996
CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: SCHIff, J. Michaeel
NAME: SCHIff, J. Michaeel
NAME: SCHIff, J. Michaeel
                                                                                                                                                                                                                                                                                                           Query Match
Best Local !
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Patent No. 6022542
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 494-079
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rose, Timothy M. APPLICANT: Bosch, Marnix L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 755 Page
CITY: Palo Alto
                                                                                                                                                                                                                                                                                        Local Similarity
les 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Morrison & Foerster STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
FILING DATE: 20-SEP-1990
                                                                                                                                                                                                                   2047 CAAACTCGTGATCCTCCAGCATG 2025
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                                                                                                                                                                                                                                                                                     64.8%;
milarity 95.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.8%; Score 21.4; 95.7%; Pred. No. 5;
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Pred. No. 5;
O; Mismatches
                                                                                      OF RECOMBINANT GLYOPROTEIN
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 921,730
; FILING DATE: 20-0CT-1986
; APPLICATION NUMBER: 597,784
; FILING DATE: 06-APR-1984
; SEQ ID NO:2:
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US-07-906-930E-1
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                                                                 Matches
                                                                                             Query Match
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Patent No. 5534631
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Best Local Similarity 95.7%;
                                                                                Best Local
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TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO:
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APPLICANT: Gaynor
                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Sertich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2517 base pairs
TYPE: nucleic acid
                                                                                                                                            MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gaynor, Richard B.
APPLICANT: Nirula, Ajay
APPLICANT: Li, Ching
TITLE OF INVENTION: DNA ENCODING THE INTERLEUKIN BINDING
TITLE OF INVENTION: FACTOR (ILF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/906,930E FILING DATE: 30-JUN-1992 CLASSIFICATION: 536
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                                                                                                                                                                              TOPOLOGY:
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                               1 CCCTGCAAACTCGTGKTCCTCCAGCATGCAGGG 33
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                                                                              Similarity
CGCTGCAAACTCCTGCCCCTCCAGCCCCCGGGG 287
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                                                                                                                                                                            linear
                                                                                                                                            other nucleic acid
/desc = "DNA"
                                                                                                                                                                                             single
                                                                              61.2%;
75.8%;
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                                                             Pred. No. 16;
0; Mismatches
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                                                                                            Length 2517;
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                                                             Gaps
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RESULT 7

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                                                                    NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Venezia, Domenick
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: RING FINGER PROTEIN ZAPOP3
FILE REFERENCE: 98-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Apr-
                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09434408 Patent No. 6440697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                      CURRENT APPLICATION NUMBER: US/09/434,408
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: US 60/108,258
EARLIER FILING DATE: 1998-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2939 base pairs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATE APPLICANT:
       TYPE: DNA
ORGANISM: Homo sapiens
EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTE: IBM PC compatible
COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,930B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                 ENGTH: 3138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SETLICH, GATY J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DNA ENCODING THE INTERLEUKIN BINDING TITLE OF INVENTION: FACTOR (ILF) NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 512-418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nirula, Ajay APPLICANT: Li, Ching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 30-JUN CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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75.8%;
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Pred. No. 16;
0; Mismatches
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                                                                                                                                                                      APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-103-840A-2
Query Match
Best Local Similarity
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                                                                                                                                         SEQ ID NO 1
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TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                          SOFTWARE: Patentin
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                                                                   LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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LOCATION: (36)
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Local Similarity 81.5%;
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58.8%;
74.2%;
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Pred. No. 7;
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Pred. No. 16
Score 19.4;
Pred. No. 72;
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                Length 4411529;
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RESULT 12 US-09-641-638-359

GENERAL INFORMATION: APPLICANT: Blumenf

APPLICANT:

Bougueleret, Lydie Chumakov, Ilya

Blumenfeld, Marta

Sequence 359, Application US/09641638 Patent No. 6432648

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CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-03-12
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SEQ ID NO 358
LENGTH: 1001
TYPE: DNA
                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 501
COTHER INFORMATION: 12-866-423: polymorphic base C or T
NAME/KEY: misc_binding
LOCATION: 482..500
OTHER INFORMATION: 12-866-423.misl
NAME/KEY: misc_binding
LOCATION: 502..521
OTHER INFORMATION: 12-866-423.mis2, potential complement
NAME/KEY: primer_bind
LOCATION: 79..98
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GENERAL INFORMATION:
APPLICANT: Blumenf
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                                                                                                               Query Match
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                                                                                             Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                    NAME/KEY: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 12-866-423 potential probe
                                                                                                                                                                                                                               OTHER INFORMATION: upstream amplification primer NAME/KEY: primer_bind LOCATION: 589.609
OTHER INFORMATION: downstream amplification primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens FEATURE:
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906
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o. 6432648
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                  CTGCAAACTCGTGKTCCTCCAGCATG 28
CTGCAAACCTGTGTTCTCCCAGCATG
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                                                                             Conservative
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                                                                                           58.2%;
80.8%;
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                                                                           Pred. No. 36; 
i Mismatches
                                                                                                                 Score 19.2;
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NAME/KEN: misc_binding
LOCATION: 502..521
OTHER INFORMATION: 12-867-47.mis2, potential complement
NAME/KEN: primer bind
LOCATION: 455..474
OTHER INFORMATION: upstream amplification primer
NAME/KEN: primer bind
LOCATION: 898..918
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEN: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 12-867-47 potential probe
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US-09-904-615-27
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                                                                           SEQ ID NO 27
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Patent No. 6566325
GENERAL INFORMATION:
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                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
                                                                                                             PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al. TITLE OF INVENTION: 49 Human Secreted Proteins FILE REFERENCE: PZ032P1
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-
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CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
                                                                                             SOFTWARE:
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              LENGTH: 1656
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 481..500
OTHER INFORMATION: 12-867-47.mis1, potential
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NAME/KEY: allele
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OTHER INFORMATION: 12-867-47 : polymorphic base C
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UMBER: US 60/133,200
1999-05-07
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Pred. No. 3
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US-08-400-159-7/c
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US-09-214-278-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 23; Conserv
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CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: sig_peptide
LOCATION: (12)..(89)
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LOCATION: (90)..(3725)
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APPLICANT:
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APPLICANT:
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                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                 TITLE OF INVENTION: NUC
TITLE OF INVENTION: SEI
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 APPLICANT:
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              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE:
                                                                                         COUNTRY:
                                                                                                                                   STREET:
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                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Ver. 2.1
                                                                                                       New York
                                                                                                                                    1155 Avenue of the Americas
                                                                                         USA
                                                                                                                                                                                                                               Mann, Robert S
Gray, Grace E.
                                                                                                                                                                                                                                                                                                         Henrique, Domingos M.P.
Lewis, Julian H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                          Fleming, Robert J.
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                              Myat, Anna M.
                                                                                                                                                                                                                                                                                                        Lewis,
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                           Ish-Horowicz, David
                                                                                                                                                      Pennie & Edmonds
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                                                                                                                                                                                   NUCLEOTIDE AND PROTEIN SEQUENCES OF THE SERRATE GENE AND METHODS BASED THEREON 20
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Pred. No. 58;
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
    nucleic search, using sw
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Maximum Match 100%
Listing first 45 summaries
    : /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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: /cgn2_6/ptodata/2/pubpna/US00_RW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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 US-09-827-688-8

US-10-027-622-39522

US-10-027-632-39523

US-09-312-762A-7

US-10-107-926A-408

US-10-198-846-4225

US-10-274-583-13

US-10-274-583-13

US-10-274-583-19

US-10-274-583-19

US-10-274-583-19

US-10-274-583-19

US-09-909-320-244

US-09-905-291A-244

US-09-905-291A-244

US-09-907-841-244

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Sequence 8, Appli
Sequence 39523, A
Sequence 39523, A
Sequence 408, Appli
Sequence 4085, Appli
Sequence 1035, Appli
Sequence 10, Appli
Sequence 244, Appli
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| | ,- | | | 19.8 | | | 19.8 | | - | • | 19.8 | | | | 19.8 | | • | • | 19.8 | ٠ | • | • | 19.8 | • | 19.8 | 9 | 19.8 | 9 |
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| US-09-905-075-244 | US-09-907-575-244 | -905-086 | US-09-905-381-244 | US-09-904-553-244 | -064 | US-09-905-056-244 | US-09-903-520-244 | | US-09-907-925-244 | US-09-904-462-244 | | US-09-907-794-244 | -902- | US-09-904-956-244 | US-09-904-119-244 | US-09-903-749A-244 | -09-902- | US-09-903-786-244 | US-09-906-700-244 | US-09-906-646-244 | US-09-904-786-244 | US-09-904-820-244 | US-09-909-204-244 | US-09-904-859-244 | -907-94 | -09-907-61 | US-09-906-838-244 | US-09-906-742-244 |
| Sequence 244, | | | | | ø | | | | | | Sequence 244, | æ | æ | ø | æ | Sequence 244, | | Sequence 244, | | | | Sequence 244, | | | | | Sequence 244, | Sequence 244, |
| App | App | Ąpp | App | ĄgĄ | ďď | ₫₫Ā | Ąpp | App | App | Āpp | đđ | ĄqA | qqA | App | App | đđ | App | App | ĄgĄ | App | App | App | App | App | App | App | Ąpp | App |

ALIGNMENTS

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RESULT 1 US-09-827-688-8

Sequence 8, Application US/09827688 Publication No. US20030165476A1

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RESULT 2
US-10-027-632-39522
; Sequence 39522, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
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APPLICANT: ORSON, FRANK
APPLICANT: KINSEY, BERMA
APPLICANT: KINSEY, BERMA
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION I
TITLE OF INVENTION: ACENTS
FILE REFERENCE: P01949US1/10004014
                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 8
                                                                                                                                                                                                                                                                                                             Query Match
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CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 154746
TYPE: DNA
ORGANISM: HERPESVIRUS
                                                                                                                                                                                        Conservative
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95.7%;
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Pred. No. 4.3;
1; Mismatches
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RESULT 3
US-10-027-632-39523
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US-10-027-632-39523
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                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILLING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-02-24
PRIOR PELLING DATE: 2000-02-24
PRIOR PELLING DATE: 1999-11-23
PRIOR PELLING DATE: 1999-11-23
PRIOR PELLING DATE: 1999-11-23
PRIOR PELLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-9
PRIOR PILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/187,363
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SOFTWARE: FastSEQ for
SEQ ID NO 39523
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Best Local :
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SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 39522
LENGTH: 639
                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR FILING DATE: 1999-08-09
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FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
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Pred. No. 4.7;
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US-09-312-762A-7/c
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                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                      Sequence 408, Application US/10007926A Publication No. US20030143539A1 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: MIA HOROWITZ ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                        APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: PERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
                                                                                                                                                                            APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOULGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION NUMBER: US/10/007,926A CURRENT FILING DATE: 2001-12-07 PRIOR APPLICATION NUMBER: 60/254;090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: 09/020
APPLICATION UNMBER: 09/020
PILING DATE: 20 FEB 1998
ATTORNEY/AGENT INFORMATION:
NAMB: Friedman, Mark M.
REGISTRATION NUMBER: 33,88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: an ASCI file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,762A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RBFBRENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TBLEFAX: 972-3-5625554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   980 TGCAAACTCGTCGTCCAGCATGC 955
                                                                                                                                                                                                                                                                                                                                                                                                                        4 TGCAAACTCGTGKTCCTCCAGCATGC 29
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/: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ½: Mark M. Friedman c/o Anthony Castorina
2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2815
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Twinhead* Slimnote-890TX
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88.5%;
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Pred. No. 4
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US-10-274-583-13/c
US-10-274-583-13/c
Sequence 13, Application US/10274583
Publication No. US20030138431A1
GENERAL INFORMATION:
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US-10-007-926A-408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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LENGTH: 3059
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Best Local Similarity
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                    OTHER INFORMATION: n = A, T, C \text{ or } G
-10-198-846-4325
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                                                                                                                                                                                                                                                                                                                                                                LOCATION: 439, 451, 525, 5;
LOCATION: 711, 715, 740, 7;
LOCATION: 812, 816, 817, 8;
LOCATION: 850, 856, 871, 8;
OTHER INFORMATION: n = A,T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: Patentin Ver. 2.1
APPLICANT: Exelixis, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 916
TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 890, 895, 896, 897, 898,
LOCATION: 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                  Local
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                                                                                                                               486 TGCAAACTGGTGGTCCACAAACATGCTTGG 515
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75.8%;
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759, 779,
826, 828,
872, 873,
87, C or G
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; Pred. No. 49;
1; Mismatches
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Pred. No. 42;
0; Mismatches
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49;
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; SEQ ID NO 9
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CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 60/38,733
PRIOR FILING DATE: 2001-10-27
PRIOR APPLICATION NUMBER: 60/357,600
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/361,196
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 24
                                                                                                                          Sequence 10, Application US/10274583
Publication No. US20030138431A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10274583 Publication No. US20030138431A1
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: LERCAPS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EXC2-119C
CURRENT APPLICATION NUMBER: US/10/274,583
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 60/338,733
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/357,600
PRIOR FILING DATE: 2002-02-15
PRIOR PRIOR APPLICATION NUMBER: 60/361,196
PRIOR FILING DATE: 2002-03-01
NUMBER: 07 SEQ. ID NOS: 24
APPLICANT: EXECUTION: LRCAPF AS MODIFIERS OF FILE REFERENCE: EXO2-119C
CURRENT APPLICATION NUMBER: US/10/274,583
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 60/338,733
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: LRRCAPS AS MODIFIERS OF FILE REFERENCE: EX02-119C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Exelixis, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3227
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3207
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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Local Similarity 84.0%;
les 21; Conservation
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mes 21; Conserv
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                                                                                                                                                                                                                                                              CCCTGCAAAGCTGTGGTCCTCCAGC
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Pred. No. 61
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Pred. No. 61
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                                                                                             THE p53 PATHWAY AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                         DB 12;
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RIOR APPLICATION NUMBER: 60/357,600

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RESULT 10
US-09-909-320-244/c
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                                      CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PPLICATION NUMBER: US 60/143,048
PRIOR PPLICATION NUMBER: US 60/145,698
PRIOR PPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-07
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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SEQ ID NO 10
LENGTH: 3227
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: williams, P. Mickey
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/361,196
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 24
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APPLICANT: Ashkenazi, Avi
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FILING DATE:
                         APPLICATION NUMBER: PCT/US99/21547
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5. US20020132240A1
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Kniher, Jennie P.
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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Botstein, David
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Filvaroff, Ellen
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Eaton, Dan L.
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Pred. No. 61
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APPLICANT: Stewart Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT PILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/143,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
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US-09-909-088B-244/c
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; ORGANISM: Homo
US-09-909-320-244
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
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Matches
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SEQ ID NO 244
LENGTH: 3679
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Best Local Similarity
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING NATE: 1000BER: PCT/US99/28564
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Mather, Jennie P...
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Pred. No. 62
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SEQ ID NO 244
LENGTH: 3679
TYPE: DNA
ORGANISM: Homo Sapien
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/21547
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                Paoni, Nicome
Roy, Margaret Ann
Chewart, Timothy A.
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Ashkenazi, Avi
Botstein, David
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          Stewart, Timo
Tumas, Daniel
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Williams, P. Mickey
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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84.0%;
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PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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LENGTH: 3679
TYPE: DNA
ORGANISM: Homo Sapien
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1999-12-20
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
                    APPLICANT:
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PRIOR FILING DATE: 1999-12-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/146,222 PRIOR FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                             1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCCTGCAAACTCGTGKTCCTCCAGC 25
                                                                                                                                                                                                                                                                                                                                                                                                          CCCTGCAAAGCTGTGGTCCTCCAGC 1273
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                                                          Fong, Sherman
Gao, Wei-Qiang
                                                                                                    Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                             Desnoyers, Luc
Baton, Dan L.
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               Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10466-14
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84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.8;
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pB 10;
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Godowski, Paul J.

Christopher J.

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RESULT 14
US-09-907-824-244/c
; Sequence 244, Application US/09907824
; Publication No. US20020197671A1
                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-853-244
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PRIOR FILING DATE: 2000-09-18
PRIOR PPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 244
LENGTH: 3679
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR FILING DATE: 1999-09-08
OR APPLICATION NUMBER: PCT/US99/20944
OR FILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/21547
OR APPLICATION NUMBER: PCT/US99/21547
OR FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                       1297
                                                                                                                                                                                                                    21,
                                                                                                                                                            1 CCCTGCAAACTCGTGKTCCTCCAGC
                                                                                                                                       CCCTGCAAAGCTGTGGTCCTCCAGC 1273
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Wood, William,
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Mather, Jennie P.
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Hillan, Kenneth, J.
                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                  60.0%;
                                                                                                                                                                                                                ; Score 19.8; D; Pred. No. 62; 1; Mismatches
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR TILING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 244
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-01
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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TYPE: DNA
ORGANISM: Homo Sapien
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                                                    LENGTH: 3679
                                                                                                                                                                                  APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
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: Ashkenazi, Avi
: Botstein, David
: Desnoyers, Luc
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Grimaldi, Christopher
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Gerritsen, Mary E.
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Ferrara, Napoleone
Filvaroff, Ellen
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Stewart, Timothy A.
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Mather, Jennie P.
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Kljavin, Ivar J.
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US-09-907-824-244

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-841-244
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                                                                                                          Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 423
SEQ ID NO 244
 Query Match
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Best Local
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 1999-11-29
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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                                                                                                                                                                                                                                                                       OR FILING DATE: 1999-07-28
OR APPLICATION NUMBER: PCT/US99/20594
OR FILING DATE: 1999-09-08
OR APPLICATION NUMBER: PCT/US99/20944
OR FILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-15
                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
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Roy, Margaret Ann
Stewart, Timothy A.
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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f, Ellen
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Other GSSB: RPCI-24-319F13.TV
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Contact: Shaying Zhao
Department of Bukaryotic Genomics
Department of Bukaryotic Research
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Teax: 301 838 0208
Email: schaoetigr.org
Clones are derived from the mouse BAC library RPCI-24.
                                                                      Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                  Bukaryota; Metazoa; Chordata;
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Levins, M.,

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                Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Chara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Kiraka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y., Sakuence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 319 row: F column: 13
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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3863 bp mRNA linear HTC 05-DEC-2002
Mus musculus adult male pituitary gland cDNA, RIKEN full-length
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Sasaki, D., Shibata, K., Shinagawa, A., Takahashi, F., Takaki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

AL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Baralov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagmer, L., Washio, T.; Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barah, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Flietcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Hofmann, M., Hume, D.A., Kaniya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Whishaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Lazarehi, P., Voshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigeronic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 420, 563-573
6 (bases 1 to 3863)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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/tissue type="pituitary gland"
/clone lib="RIKEN full-length
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                                                                              /clone="5330415G09"
                                                                                                                                                                                                                                                                                                                              gtrain="C57BL/6J"
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                                                                                                                                              sex="male"
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                                                         enriched mouse cDNA library"
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RESULT 3
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,Y.S., Kim,Y.S.
                                                                                                                                               23;
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AA972967 605 bp mRNA linear EST 07-JU op25d11.sl Soares NFL T GBC_S1 Homo sapiens cDNA clone IMAGE:1577877 3' Similar to TR:014611 014611 HPAST.; contains
                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 Eoeun-dong Yuseong-gu,
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: !
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: yongsung@mail.kribb.re.kr
Plate: 37 row: E column: 05
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CB159107
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K-EST0218577 L18POOL1n1 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kim YS
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                                                                                                                                                                                                                                /note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell
                                                                                                                                                                                                           culture."
                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                  'lab_host="Top10F'"
'clone_lib="L18POOL1n1"
                                                                                                                                                                                                                                                                                                                           clone="L18POOL1n1-37-B05"
cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
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81.2%;
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09-MAY-2003
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Query Match
Best Local Similarity
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                Homo sapiens (human)
                                                                                                EST; expressed sequence
                                                                                                                                           Homo sapiens mRNA; EST DKFZp779E0170_r1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 932 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          element TAR1 repetitive element ;, AA972967 AA972967.1 GI:3148147
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EuKaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 605)
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                                                                                                                                                                                                                                                                                                                                                                    standard; RNA; EST; 639
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/note="Torgan: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
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/mol_type="mRNA"
/db_xref="taxon:9606"
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lab_host="DH108"
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75,
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Pred. No. 4.5e+02;
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                                                                                                                                              clone DKFZp779E0170)
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                           Euteleostomi; Mammalia;
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                                                                                          FEATURES
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Best Local S
Matches 23
                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.

No s1 sequence available.

This clone (DKFZP779E0170) is available at the RZPD in Berlin.
This clone (DKFZP779E0170) is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 639 BP; 160 A; 171 C; 194 G; 114 T; 0
                                                                        source
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M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278
                                                                                                                 Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: C column: 09
                                                                                                                                                                   Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                            Kim, N.S., Hahn, Y., Oh
Oh, K.J., Cheong, J.E.,
Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 639)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R
                                                                                                                                                                                                                                                                                                                                                                                                                     CB155818
CB155818.1 GI:28140931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-EST0214333 B2N807043 Homo
                                                                                                                                                                                                                                   Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiene
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                                                                                       quality sequence stop: |
Location/Qualifiers
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/organism="Homo sapiens"
/organism="Homo sapiens"
/clone="DKFZp779E0170"
/clone_lib="779 (synonym: hnccl). Vector pSportl_Sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="fetal"
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              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xrefs"taxon:9606"
/clone="B2N807043-16-C09"
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/moI_type="mRNA"
/sex="M"
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Pred. No. 4.6e+02;
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D-85764 Neuherberg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA line
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g, GERMANY
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B2N807043-16-C09 5',
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RESULT 7
CA488926/c
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                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 884)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM14281 row: m column: 04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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/clone lib="B2N807043"
/clone lib="B2N807043"
/note=Torgan: Brain; Vector: pCNS-D2; Site_1: EcoRI;
/note=Torgan: Brain; Vector: pCNS-D2; Site_1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatese (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
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/clone_lib="MAPCL" | /clone_lib="MAPCL" | /clone="Vector: pCMV-SPORT6; Site_l: BcoRV; Site_2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast
                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6721132"
                                                                                                                                                                                                                                  /cell_line="ZR-75-1,
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88.5%;
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Pred. No. 4.6e+02;
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GE:6721132 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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Seq primer: -21M13UnivRev
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 bp DNA 1: 1659g07.g1 WGS-ZmaysF (DH5a methyl filtered) 1659g07.5', genomic survey semianon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mccombie@cshl.org
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516 367 8874
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                                                                                                                                                                               /clone lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleoTide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (.x/y
reads in M13mpl9, .b/g reads in pUCl9). The same ligation
was transformed into DH5a."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer genes encoding membrane Manuscript submitted."
231 c 216 g 199 t
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/mol_type="genomic ro
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/clone="ie59g07"
                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA'
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH5a"
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                                                                                      67.3%;
82.8%;
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88.5%;
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                                                                      Score 22.2; DB 29;
Pred. No. 5.7e+02;
1; Mismatches 4;
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Pred. No. 5.1e+02;
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                                                                      Gaps
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COMMENT

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

construction of a

Genome Res.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 157-1771 (2000)

TITLE

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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nkazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nkaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., L.B., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gassterland, T., Gariboldi, M., Gissi, C., Gorbani, L.B., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Vangis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, E.D., Kanai, A., Kawaji, H., Marchoni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Kingwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watensbe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakazume, M., Sainsaki, D., Shibata, K., Shibasta, J., A., Sasaki, D., Shibata, K., Shibasta, J., A., Sakazume, M., Sasaki, D., Shibata, K., Shibasta, J., A., Sasaki, D., Shibata, S., Hara, A., Hashizume, W., Imotani, K., Ishii, M., Kayana, J., A., Shibata, Y., Sasaki, D., Shibata, S., Hara, A., Hashizaki, Y., Waterston, R., Lander, S., Shibasta, S., Shibasta, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., 
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Maki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY540314 RIKEN full-length enriched, B6-derived CD11 +ve de cells Mus musculus cDNA clone F730006E21 3', mRNA sequence.
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Eukaryota, Metazoa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12466851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                         Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 401)
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Rodentia;
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d, B6-derived CD11 +ve dendritic
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SOURCE
ORGANISM
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BY541787/c
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                                                                                    Nikaido, I., Osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Pletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinoich, S., Hitokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., P.A., Maglott, D.R., Maltais, L., Marchiomni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., P., Setou, M., Sahanda, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teadale, R.D., Tomita, M., Sandelin, A., Schnider, C., Semple, C.A., Setou, M., Sahmada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teadale, R., Wang, I., Yang, I., Yang, L., Yang, L., Wan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakazume, N., Sayawa, I., Miyazaki, A., Sakai, R., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, S., Shibata, T., Barai, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, J., Banai, K., Sasaki, D., Shibata, K., Sasaki, D., Sakai, S., Sasaki, D., Shibata, K., Sasaki, D., Sakai, S., Sasaki, D., Shibata, K., Sasaki, D., Sakai, S., Sasaki, D., Sabata, 
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
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405 bp mRNA linear EST 14-DEC-200:
BY541787 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
cells Mus musculus cDNA clone F730022F15 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 405)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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/clone_lib="RIKEN full-length enriched, B6-derived CD11
+ve dendritic cells"
105 c 106 g 100 t
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                                                                      functional annotation
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                                                                         SOURCE
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AUTHORS

ACCESSION

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Query Match
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                                                                                                                                                                                                                                                              87536425 ATKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630310H17 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust (MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Sakai,K.,
Murata,M., Nakamura,M., Nomura,K., Nhbata,K., Shiraki,T., Tagami,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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78.1%;
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Gustincich,S., Hirokawa,N., Jackson,I.J., Tarvice,F., K., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Tarvice,F., Gondani, G., Gustincich,S., Hirokawa,N., Jackson, G., Gustincich,S., Hirokawa, M., Jackson, G., Gustincich, G., Gustincich,
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Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishi, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
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                                                                                                                                                                                                                                                                                                                                                                              Please visit
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okazaki,Y., Furumo,M., Kasukawa,T., Adachi,J., Bono,H., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach, Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY535446 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630305G21 3', mRNA
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                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                 Nature 420,
22354683
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T.,
                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                           Fax: 81-45-503-9216
                                                                                                                       Tel: 81-45-503-9222
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/cell type="NOD-derived CD11c +ve dendritic cells"
/clone lib="RIKEN full-length enriched, NOD-derived type dendritic cells"
+ve dendritic cells"
116 c 122 g 104 t
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/db_xref="taxon:10090"
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Pred. No. 5
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   Carninci, P., Fukuda, S., Hirozane
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RESULT 13
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                                                                              1 (bases 1 to 643)
1 (bases 1 to 643)
1 (bases 1 to 643)
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulat Vascular Plants. Project: 1024b
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BI528489

BI624091A09 yl C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.

BI528489

BI528489.1 GI:15369063

BST.
Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
DCMB Box 91000
Duke University
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10 (11), 1757-1771 (2000)
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                                                          Contact: Charles Hauser
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/clone="F630305G21"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 651)
Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                 DCMB Box 91000
Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                            Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular Plants. Project:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B1528424 1024090E05.yl C. reinhardtii CC-1690, normalized, Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                            chauser@duke.edu.
                                                                                                                                                                                                                                                                                                                                            NC 27708-1000
                /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines_cDNAs from CC-1690 cells grown to
mid-log phase in
                                                                                                                                  /organism="Chlamydomonas reinhardtii"
/mol_type="mENA"
/strain="CC71690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
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                                                                                                               /clone_lib="C.
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78.1%;
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; Pred. No. 6.5e
1; Mismatches
                                                                                                          reinhardtii CC-1690, normalized, Lambda Zap
(acetate-containing)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shaying Zhao, William Nierman, Mark Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CCTGCAAACTCGTGKTCCTCCAGCATGCAGGG 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are darived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

BACPAC Gesources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Map Building
Unpublished
Other GSSs: RPCI-11-452E3.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 398)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
a 117 c 98 g 101 t 9 others
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/mol_type="genomic DNA"
/db_xref="GDB:7673282"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                              sex="Male"
                                                                                                                                                                                                                                                                  clone="RPCI-11-452E3"
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82.1%;
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78.1%;
Score 21.8; DB 28;
Pred. No. 6.7e+02;
1; Mismatches 4;
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1; Mismatches 6
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Homo sapiens genomic clone RPCI-11-452E3,
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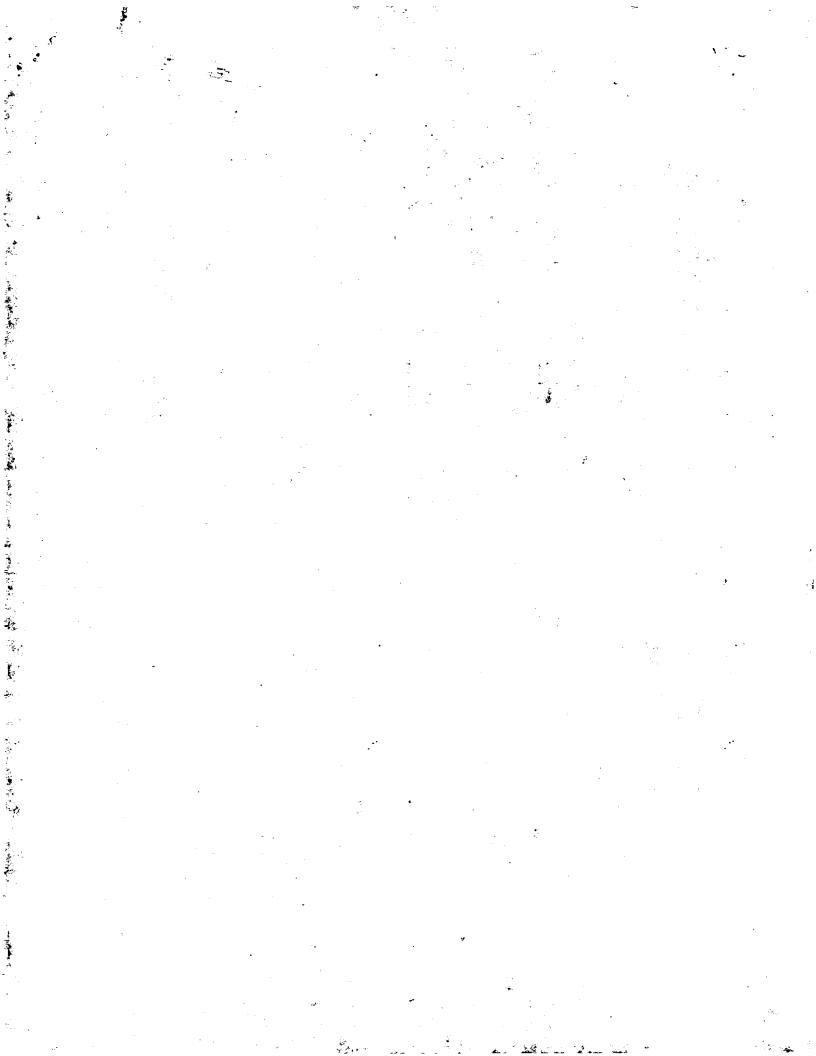
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104 CCCTGCAACCCCCTGGTCCTCCAGCANG
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Search completed: September 16, Job time: 1674.26 secs 2003, 20:40:01



Run 8

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Post-processing:
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298741.1 GI:2342602
298741.1 GI:2342602
30S ribosomal protein S15; ABC-type transporter; aminomethyl transferase; aminopeptidase; branched-chain amino acid aminotransferase; cobr; cysE; cysE; cysteine synthase; dihydrolipoamide succinyltransferase; gcvT; gpsI; guanosine pentaphosphate synthetase; ilvE; lipA; lipB; lipoate-protein ligase; lipoic acid synthetase; major membrane protein I; mmpI; multifunctional enzyme;
nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransf*,
nif5-like protein; oxidoreductase; pepA; polyribonucleotide
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Pred.

No.

16

the number of results predicted by chance to have

a

40281 bp cosmid B22.

linear

BCT

22-AUG-1997

Database

Maximum Minimum Total number Searched:

DB seq

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length 1.7 263091 1.7 267991 1.7 267991 1.7 270706 1.0 182462 1.0 18 7 92019 7 94244 7 110000 7 113454 194985 200548 163132 68974 몂 AC118318 AC120822 AC129862 AC129862 AC092669 AC003090 AC003090 AC018646 AC128646 AC128646 AC128646 AC138342 AC138342 AC12934 AC002315 AC121312 AC117138 AC117138) AC002406) AL672026 AC126569 AC113777 AC003656 AC017944 AP001054 HSA340406 HSA339685 HSA340046 HSA340037 HSA340033 AL450320 AC063938 AC107570 BX510361 MLEPRTN4 AE003979 AE012555 LMFLCHR34_04 AC074063 Ħ BX294168 ALIGNMENTS AL450320 Human DNA AC063938 Homo sapi Continuation (7 of AC017944 Drosonhi Continuation (5 of ACC)74063 Mus muscu ACC)74063 Mus muscu ACC)71312 Mus muscu ACC)71312 Mus muscu ACC)7138 Rattus no ACC)26569 Rattus no ACC)2777 Rattus no ACC)7570 Rattus no BX294168 Mus muscu ACC)7570 Rattus no BX210361 Mus muscu ACC)7579 Rattus no ACC)28962 Rattus no ACC)28962 Rattus no ACC)28964 Rattus no ACC)28964 Rattus no ACC)28964 Rattus no ACC)28965 Rattus no ACC)28965 Rattus no ACC)28964 Rattus no ACC)28965 Rattus no ACC)28965 Rattus no ACC)28965 Rattus no ACC)28664 Rattus no ACC)28667 Rattus no ACC)28667 Rattus no ACC)28668 Rattus no ACC)3986 Rattus no ACC)39 AC116818 Mus muscu AC138342 Mus muscu AC129934 Mus muscu AC125157 Mus muscu AC098887 Mus muscu AX122231 BD164348 AJ340406 AJ3400037 AJ340037 AJ340033 AL450320 AC063938 AL583920 Mycobacte AE003979 Xylella f AE012555 Xylella f AP001054 Description Z98741 Mycobacteri Sequence Novel pol Homo sapi Homo sapi Homo Homo Homo

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gene
                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                         Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                              are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. All CDS over 100 codons have been analysed. Gene prediction is based on positional base preference in codons especially where there is an increase in the observed/expected third position G + C. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we arrange for a small overlap between neighbouring submissions. Cosmid B22 is overlapped by B1551 at the 5' end, and by B129 at the 3' end. There are at least 9 conflicts between this sequence and the previously published sequences; in each case our sequence has been checked and is thought to be correct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Details of M. leprae sequencing at the Sanger Centre are available on the World Wide Web.
On the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/)
CDS are numbered using the following system eg MLCB33.01c. ML (M. leprae), cB33 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Sanger Centre is funded to complete the sequence of M. leprae by the Heiser Program for Research in Leprosy and Tuberculosis of The New York Community Trust.

Work in Paris is supported by the Heiser Trust, the Association Francaise Raoul Pollereau and the Groupement de Recherches et des Etudes des Genomes (GIP-GREG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Notes:
The Sa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium leprae
Mycobacterium leprae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biglmeler, K., Honore, N., Woods, S.A., Caudro
Use of an ordered cosmid library to deduce
of Mycobacterium leprae
Mol. Microbiol. 7 (2), 197-206 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strand).
The more significant matches with motifs in the PROSITE database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (kei@pasteur.fr)
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riboflavin kinase; RLEP; RLEP2; rpsO; serine acetyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 40281)
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                                     complement (1. .7427)
/note="overlap with EM_BA:MLB1551CS L78813 Mycobacterium leprae cosmid B1551 from: 2 to: 7425"
                                                                                                                                                                                                         /clone="cosmid B22"
                                                                                                                                                                                                                                                                                                                                                         organism="Mycobacterium
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                                                                                                                                                                                                                                                               xref="taxon:1769"
                                                                                                                                                                                                                                                                                                                    type="genomic DNA"
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/trans1_table=11
/product="hypothetical prote
/protein_id="CAB11366.1"
/db_xref="GI:2342603"
/db_xref="SPTREMBL:032951"
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complement (566. .670)
/note="MLCB22.03c, probable pseudogene fragment, len:
/n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MLCB22.02c, probable pseudogene fragment, len 64 aa; similar to part of Y00G MYCTU Q10394 hypothetical 48.6 kd protein cy190.16 (480 aa) (57.8% identity in 64 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MLCB22.01c"
/note="MLCB22.01c"
/note="MLCB22.01c, unknown, partial CDS, len >66 aa;
/note="MLCB22.01c, unknown, partial CDS, len >66 aa;
/note="MLCB22.01c, unknown, partial CDS, len >66 aa;
/note="MLCB22.01c"
/note=
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/note="MLCB22.04c, probable pseudogene fragment, len:
aa; similar to part of Y00g MYCTU Q10394 hypothetical
kd protein cy190.16 (480 aa) (75.0% identity in 20 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MLCB22.06c, probable pseudogene fragment, len:
aa, similar to part of Y00G MYCTU Q10394 hypothetical
kd protein cy190.16 (480 aa) (63.3% identity in 30 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /pseudo
/codon_start=1
/transl_table=11
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aa; similar to aprt of YOOG_MYCTU Q10394 hypothetical
kd protein cy190.16 (480 aa) (63.0% identity in 27 aa
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/db_xref="PID:e335006"
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/transT_table=11
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/db_xref="PSEUDO:CAB11368.1"
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ggcaglrynlppddrtldgdlt"
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/transI_table=11
/db_xref="PID:e335008"
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/transl_table=
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/gene="MLCB22.07"
/note="MLCB22.07,
C- terminus to M.
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unknown, len: 247 aa; highly similar tuberculosis YOOH_MYCTU Q10395 very
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REFERENCE
AUTHORS
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LOCUS
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Mycobacterium leprae strain TN c
AL583920 AL450380
AL583920.1 GI:13092022
                      1 (bases 1 to 346450)
1 (Cole, S.T., Eiglmeier, K., Parkhill, J., James, K.D., Thomson, N.R., Wheeler, P. R., Honore, N., Ganier, T., Churcher, C., Harris, D., Wheeler, P. R., Honore, N., Ganier, T., Churcher, C., Harris, D., Mungall, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R. M., Detvlin, K., Duthoy, S., Feltwell, T., Fraser, A., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Lacroix, C., Maclean, J., Moule, S., Murphy, L., Oliver, Quail, M.A., Maclean, M.-A., Rutherford, K.M., Rutter, S., Seeger, K., Simon, S., Simonds, M., Skelton, J., Squares, R., Squares, S., Stevens, K., Taylor, K., Whitehead, S., Woodward, J.R., and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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Mycobacterium leprae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Massive gene decay in the leprosy bacillus
                                                                                                                                                                                                                                                                                              Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MLCB22.08, cobT, probable
/incotinate-nucleotide--dimethylbenzimidazole
phosphoribosyltransferase (component of the cobalamin
biosynthesis pathway), len: 351 aa; similar to many eg.
COBT_ECOLI P36562 nicotinate-nucleotide--dimethylbenzimida
zole phosphoribosyltransferase (BC 2.4.2.21) (359 aa),
fasta scores; opt: 616 z-score: 753.3 E(): 0, 34.8%
identity in 345 aa overlap. Also highly similar to M.
tuberculosis cobT, MTCY190.18 (81.4% identity in 355 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="conflict: this base is missing in EM_BA:MLB1554CS
L78814 Mycobacterium leprae cosmid B1554"
2311. .3366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphoribosyltransferase"
/protein_id="CAB11373.1"
/db_xref="GI:2342605"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overlap) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="cobT"
2311. .3366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mrahasgqpicrrsslaivkligrkksygqdietsddnygseas
LPDTLSRGSSTTAPKGRPTRKRDDADRRHTKKGPITPAPMTASEARARRKSLAPPKCH
RAERRAKRAASKAQITDRRERMMAGEEAYLPPRDQGPVRRYIRDLVDARRNALGLFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALVLLFITFGVPQLQLYMSPAMLVLLSVMGIDGIILGRKISKLVDVKFPSNTESHWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scores; opt: 66:
124 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGQCPPRQFQRARIVVFAGDHGVARSGVSAYPPQLTAQMVANIDRGGAAINALASIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transI_table=11
/product="nicotinate-nucleotide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGLYAAGRASQMRRLRVPRPQVEHGSSVG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nypothetical 14.0 kd protein cy190.17 (124 aa), fasta scores; opt: 661 z-score: 1033.3 E(): 0, 76.6% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="Sptrembl:032953"
translation="MEFAPVSPPDGHAAAAARARQDTLTKPRGALGRLEDLSIWVASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.7%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20.6; DB 1;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 protein MLCB22.07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome; segment 4/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 40281;

    dimethylbenzimidazole

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCT 20-FEB-2001 .
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MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                  gene
                                                                                                                                                                                           RBS
                                                                                                                                                                                                                                                                                                                                                                                                             gg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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21128732
11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of M. leprae sequencing at the Sanger Centre are available from http://www.sanger.ac.uk/Projects/M_leprae/ A relational datbase containing the M. leprae sequences is available from http://genolist.pasteur.fr/Leproma/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-PEB-2001) Submitted on behalf of the Mycobacterium
Submitted (20-PEB-2001) Submitted on behalf of the Mycobacterium
leprae sequencing teams, The Sanger Centre, Wellcome Trust Genome
Campus, Hinxton, Cambridge, CB10 1SA, UK Unitie de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Rouu
75724, Paris Cedex, France. E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
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ADFFVESGHKIYGFTGIGVLYGCEDVLTEMPWQGGGNMIUDVTLERSLYQGPNKFE
AGTGNIADAVGLGEALRYVERVGVQRIASHEQALLDYATPRLADIPGVRLVGTATEKA
SVLSFYLAGHEPLEVGKALNAEGIAVRAGHHCAQPVLRRLGLEATVRPSFAFYNTYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Similar to Mycobacterium tuberculosis hypothetical 44.6 kp protein Rv1464 or MTV007.11 TR:05315 kg. 43.6% id in (EMBL:ALO21184) (417 aa) fasta scores: E(): 0, 43.6% id in 408 aa and to many other bacterial nifs-homologues, e.g. Bacillus subtills YurW protein yurW TR:032164 (EMBL:Z99120) (406 aa) fasta scores: E(): 0, 46.7% id in 405 aa. Previously sequenced as TR:032975 (EMBL:Z98741). Contains Pfam match to entry PF00266 aminotran_5,
                      2559. .4112
/gene="ML0844"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Pfam match to entry PF00266 aminotran 5, Aminotransferases class-V, score 23.70, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDVFINVVRRIAEGGTNIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aminotransferases class-V.
Similar to ML0117, ML0596
                                                                                                                                                                                                            /codon_start=1
/transl_table=11
/product="lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="ML0842"
note="Similar to Mycobacterium tuberculosis putative
                                                                                                                                                               'note="possible RBS"
                                                                                                                                                                                                                                                                                                                                               note="ML0843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="ML0843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="ML0842"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="ML0842"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mycobacterium leprae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                         note="synonym: nark"
                                                                                                           gene="ML0844"
                                                                                                                                                                                                                                                                                                                                                                                                                                       pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (6823), 1007-1011 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _xref="taxon:1769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .348450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type="genomic DNA"
                                                                                                                                                                                                                                                                                                                           (Best blastx
                                                                                                                                                                                           2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                        lppp"
                                                                                                                                                                                                               (pseudogene) "
                                                                                                                                                                                                                                                                                                                           ene of M. tuberculosis orthologue 294)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and ML1708"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score 23.70, E-value 1.7e-08*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 rue du Docteur Rouux,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trust Genome
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밁 S

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FWGGRLADRLGGSSYLNTGGVFAAFWIFMLCYAAAGVLTWKMYVCRPLPGNLHDEAANAFAAS
GTBLLALRESYLNTGGVTAAFWIFMLCYAAAGVLTWKMYVCRPLPGNLHDEAANAFAAS
GTBLLALRESYLNTGGVTAAFWIFMLCYAAAGVLTWKMYVCRPLPGNLHDEAANAFAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ML0845"
/note="Unknown function. Similar to part of some acyl-Co-
/note="Unknown function. Similar acyl-CoA oxidase cx2
oxidases e.g. Arabidopsis thaliana acyl-CoA oxidase cx2
TR:065201 (EMBL:AF057043) (692 aa) fasts scores: E():
TR:065201 (EMBL:AS90741) (193 aa) fasts scores: E(): 0,
99.5% id in 193 aa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nitrite extrusion protein narK1 or Rv2329c or MTCY3G12.05 TR:P71883 (RMBL:Z79702) (515 aa) fasta scores: E(): 0, 69.3% id in 488 aa and to Escherichia coli nitrite extrusion protein 2 narU SW:NARU ECCLI (P37758; P77696) (462 aa) fasta scores: E(): 0, 36.6% id in 459 aa. There is a frameshift near the C-terminus relative to the M. tuberculosis homologue. Previously sequenced as TR:032974 (EMBL:Z98741). Contains hydrophobic, probable membrane-spanning regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tranalation="MPLRPTNAASERVTKRTATETILQRMVGARQDSKKGSLENRGT
QGTIFEKCEDCLLSAVARRRQVKSKEMFAFDTFNTVQDHLLHAANEHTDRVVLETFLA
GIESCKUDPAARKLLDIVCDLYALSVKARHGTSSIDTSPESALKAIAKGSRPMPSAAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/product="ABC transporter
complement(5522. .5848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ML0845"
complement (4100, ,4681)
                                                                                                                                                                                 /gene="ML0848"
5906. .8080
                                                                                                                                                                                                                                                     /codon_start=1
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/product="conserved
5906. .8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4959. .5480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ML0846"
/pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4100. .4681)
/note="Similar to Mycobacterium tuberculosis hypothetical ABC transporter ATP-binding protein Rv326c or MTCY3G12.08 SW:YN26 MYCTU (P71886) (697 aa) fasta scores: E(): 0,76.9% id in 697 aa. Shares similar domains with many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (5522. .5848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             paralogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=;
/transl_table=
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/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Possible pseudogene of M.
Rv2327 (Best blastx score 184)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Possible pseudogene similar to M. tuberculosis
paralogue Rv1747 (Best blastx score 127)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ML0846"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="ML0847"
                                                                                                                                             gene="ML0848"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="ML0847"
                                                                                                                                                                                                                                                  . 8080
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                                                                                                                                                                                                                                                                               hypothetical protein (pseudogene) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (pseudogene) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis orthologue
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gene

CDS

gene

RESULT 3 AB003979

FOCUS

KEYWORDS

ð 밁

Matches

Sd

gene

Sg

JOURNAL MEDLINE

PUBMED

TITLE

gene

CDS

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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
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ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                                                                                                                                                                                                             Simpson, A.J., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvarenga, R., Alves, L.M., Araya, J.E., Baia, G.S., Baptista, C.S., Alvarenga, R., Bonaccorsi, B.D., Bordin, S., Bove, J.M., Briones, M.R., Bueno, M.R., Camargo, A.A., Camargo, L.E., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costa, P.F., Costa, M.C., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias.Neto, B., Docena, C., El-Dorry, H., Facincani, A.P., Ferreira, A.J., Perreira, V.C., Ferro, J.A., Praga, J.S., Franca, S.C., Franco, M.C., Fohme, M., Furlan, L.R., Garnier, M., Goldman, G.H., Goldman, M.H., Gomes, S.L., Gruber, A., Ho, P.L., Hoheisel, J.D., Junqueira, M.L., Kemper, B.L., Kitajima, J.P.
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                                                         and Marino, C.L.
The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylella fastidiosa 9a5c
Xylella fastidiosa 9a5c
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB003979 11282 bp DNA linear BCT 15-UNV-2001 Xylella fastidiosa 9a5c, section 125 of 229 of the complete genome. AB003979 AE003849 AE003979.1 GI:9106520
10910347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGCGTAGTGGTACGACCTCCTGCAG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTAAGTAGTGGCAAGACCTCCTGCAG 5102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 11282)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trainibation="MOLCIHRAMALLCQATRRCHRWKTQLGRCAAPDLAPGTGTIGKV
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PALAKRRIDGLSGGGMRVVLAGLLACSPRALILDEPLAGLDAVSQRGLLRLLEDLRC
PRALAKRRIDGLSGGGMRVVLAGLLACSPRALILDEPLAGLDAVSQRGLLRLLEDLRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ML0848"
/note="Pfam match to entry PF00005 ABC_tran,
transporter, score 112.30, E-value 9e-30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6821. .7336
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85.2%;
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Pred. No. 1
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REFERENCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 11282)
Simpson,A.J.G., Reinach,F.C., Arruda,P., Abreu,F.A., Acencio,M., Alves,L.M.C., Araya,J.E., Baia,G.S., Baptista,C.S., Barros,M.H., Bonaccorsi,S.D., Bordin,S., Bove,J.M., Briones,M.R.S., Bueno,M.R.P., Camargo,A.A., Camargo,L.B.A., Carraro,D.M., Carrer,H., Colauto,N.B., Colombo,C., Costa,F.F., Costa,M.C.R., Costa-Neto,C.M., Coutinho,L.L., Cristofani,M., Dias-Neto,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-2000) Organization for Nucleotide Sequencing and Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas, SP
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                                                                                                                                                                                                                                             /translation="midnnvlmldaiaeakyklteelrrleeqevqllqqqaaemftr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to GI|1360644 (percent identity: 46 %/query alignment coverage: 96.4 % subject alignment coverage: 100.0 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="XF1493"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein; identified by sequence
similarity; putative; ORF located using Glimmer/RBSfinder"
/note="similar to GI|2121183 (percent identity: 26 */query
alignment coverage: 93.6 */subject alignment coverage:
102.6 *); identified by sequence similarity; putative; ORF
                                                                                                                                                                           complement (2605. .3492)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MHYHCAPSFSPALLLSVRTAIKSDHQSNIILAVWRHGKTEIDIP
KQKYDIVYEKFGKKLNEAFQPATATK"
                                                                                                                                       complement (2605. .3492)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (205. .417)
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                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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/db_xref="GI:9106522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="XF1492"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                              /""
alignment coverage: 100.4 */subject alignment coverage:
97.5 *); identified by sequence similarity; putative; ORF
located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDVTVYANWGRTFQIGSGNGAYRTQADDLVPSMNDGWETGLTFKPWSWANARLVYWQQ
RASGEVATLFGTNGAIAINEVGNVGKTLRNGWDAQLNLQPDEQWRVWLAYSRQKAEIA
IPDPSVPATRGKQIENVPRWLTNVGAEWQVLPKLKLSAWGNGQGNYYVERTNTLGRYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHARAIKRAVSGKWGYADPRDAWRAGLSVRYFHNDAQEPGYLTYDAAVADPRSSPAYS
GQHEGQCTVCTALHLDGRWSBAPHWTAKAYIKRYTNDRVVKFYAASARQERYTDETH
RGVLTINAIWRESVDWYHEFSLEGGVUDAQWQSNVSRKYKHLDGQRGTVLRADDEPKLDY
GAYLQAVIRVNDSLKLVPAYRVDRIDGRFSDIASGLRYPVYRYGTIQQPKFSVSYDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPSFRCPFSVSLPSLILCSVVFGVHATAVTTSTDHSLPLSLGKI
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NAIAGHVDVITRSGGNDGLLSVTTGDFGTRKIQMVKGIERGAMSQNYVVSWLDSDGYR
IVQQRDERYKISPIADWTDRDIWEYMKHHDLPYHPLWEQGYVSIGDIHTTRPLEPGW
EEDTRFFGFKRECGIHENI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYFLSNLSATWILSNKSELTLQLNNVTNRFYVYAWYDSGLSGYSPGDGRALYLTWNLI
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/gene≈"XF1495"
                                                              awtearhgrlweqgidginqyntlhkvepmrralbelqvgtwftglrrgqsstrtqts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (6796. .7509)
/gene="XF1497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (6796 .7509)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="TonB-dependent receptor for iron transport"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment coverage: 77.5 %/subject alignment coverage
75.6 %); identified by sequence similarity; putative;
located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGEACPPYPSNAPVRYVLELNAGQAARLDLKDGTQLVFGPGIPKL"
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YDPRNSYLKQVPERRIGNPISLAVIQIEVARRIGIPLGGVSPRGHFLVRLFVDDGIIV
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NIVNHWDRAARCADRILKLVPNQPEALRDRGIAYLQIGHRSGARNDLTRYLQLYPSTHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="conserved hypothetical protein"
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db_xref="GI:9106524"
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transl_table=11
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'gene="XF1496"
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db_xref="GI:9106523"
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                                                                                                                                 JOURNAL
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18 Van Sluys, M.A., de Oliveira, M.C., Monteiro-Vitorello, C.B., Miyaki, C.Y., Furlan, I.R., Camargo, L.B.A., da Silva, A.C.R., Moon, D.H., Takita, M.A., Lemos, E.G.M., Machado, M.A., Ferro, M.I.T., da Silva, F.R., Goldman, M.H.S., Goldman, G.H., Lemos, M.V.F., El-Dorry, H., Tsai, S.M., Carrer, H., Carraro, D.M., de Oliveira, R.C., Nunes, L.R., Siqueira, W.J., Coutinho, L.L., Kimura, E.T., Ferro, E.S., Harakava, R., Kuramae, E.E., Marino, C.L., Giglioti, E., Abreu, I.L., Alves, L.M.C., do Amaral, A.M., Baia, G.S., Blanco, S.R., Brito, M.S., Cannavan, F.S., Celestino, A.V., da Cunha, A.F., Fenille, R.C., Perro, J.A., Formighieri, E.F., Kishi, L.T., Leoni, S.G., Oliveira, A.R., Rosa Jr., V.E., Sassaki, F.T., Sena, J.A.D., de Souza, A.A., Truffi, D., Tsukumo, F., Yanai, G.M., Zaros, L.G., Civerolo, E.L., Simpson, A.J.G., Almeida Jr., N.F., Setubal, J.C. and Kitajina, J.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xylella fastidiosa Temeculal
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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Xylella fastidiosa Temeculal,
                                                       Van
                                                                                                                                                                              Comparative Analyses of the Complete Genome Sequences of Pierce's Disease and Citrus Variegated Chlorosis Strains of Xylella
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                                                                                                       12533478
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(bases 1 to 302835)
n Sluys,M.A., de Oliveira,M.C., Monteiro-Vitorello,C.B.,
yaki,C.Y., Furlan,L.R., Camargo,L.E.A., da Silva,A.C.R.,
yaki,C.Y., Takita,M.A., Lemos,B.G.M., Machado,M.A., Ferro,M.I.T.,
                                                                                                                              Bacteriol. 185 (3),
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ptgalhesdqtikkngsqoddrdleerreqkleraygemirthggw
LOLDAIATRYANHSLRVTTROARGPHOVIKELKATMQAINAALIDTLAAGGDVRNW
QVAANPLLSRAHADLYTDAAHLSEHLLENTRAYYEIWLDEKKVAGAGEEEEPIYGPHY
LPRKEKIGFAAPPINDUVPFANDLGFIAVIVNTLLGYNVAIGGMGTTHGDPDTWPR
VGNIIGFITRADLIAISTAIVTQRDFGWRTLKKRARFKYTIDDRGLDCIVGEIQQRA
GITLQPAAPPVFEHNGDRYGWIEGEDRHWHLTLSLPAGGRATADTESSPLLGFRAIAQRA
GITLQPAAPPVFEHNGDRYGWIEGEDRHWHLTLSLPAGGRATADTESSPLLGFRAIAQRA
GITLQPAAPPVFEHNGDRYGWIEGEDRHWHLTLSLPAGGRATADTESSPLLGFRAIAQRA
GITLQPAAPPVFEHNGDRYGWIEGEDRHWHLTLSLPAGGRATADTESSPLLGFRAIAQRA
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GRYNLMLGGDQRGQRLNTLYRENITETEILAALEPLLGRYQQKRLPGEGFGDFLHRTG
IIALPPYPTHRHVISSTLQA"
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/gene="XF1499"
complement (9336. .11174)
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/protein id="AAF84307.1"
/db_xref="GI:9106527"
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Pred. No. 1.7e
0; Mismatches
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                                                  /translation="mirfatagffyvlltpmvkastphysvntpfnqstptttvvtpin
Tmpynpqtplgipgkalsqrynreylmdpmllhlrvnsrqsiaktkttstestansnn
Ktetdykkqtiydntpmrfnmnqqgkkmtadefdammkargvhvipsqtnnnvqsvse
ak"
                             complement (5836.
                                                                                                                                                                                                                                                                                                                                     complement (4427. .4915)
/locus_tag="PD0503"
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/locus_tag="PD0504"
                                                                                                                                                 product="conserved hypothetical protein"
protein_id="AAO28378.1"
/db_xref="GI:28056499"
                                                                                                                                                                                                                                codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                   notes identified by sequence similarity; putative; ocated using Blastx/Glimmer"
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da Silva, F.R., Goldman, M.H.S., Goldman, G.H., Lemos, M.V.F., Bal, Dorry, H., Tsai, S.M., Carrer, H., Carraro, D.M., de Oliveira, R.C., Nunes, L.R., Siqueira, W.J., Coutinho, L.L., Kimura, E.T., Ferro, E.S., Harakava, R., Kuramae, B.E., Marino, C.L., Giglioti, B., Abreu, I.L., Alves, L.M.C., do Amaral, A.M., Baia, G.S., Blanco, S.R., Brito, M.S., Cannavan, F.S., Celestino, A.V., da Cunha, A.F., Fenille, R.C., Ferro, J.A., Formighieri, E.F., Kishi, L.T., Leoni, S.G., Gliveira, A.R., Rosa, Jr., V.B., Sassaki, F.T., Sena, J.A.D., de Souza, A.A., Truffi, D., Tsukumo, F., Yanai, G.M., Zaros, L.G., Civerolo, B.L., Simpson, A.J.G., Almeida Jr., N.F., Setubal, J.C. and Kitajima, J.P.
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NTEGOPYDESCHPLANSDRGYVEVSVRVKVCDASVGLESNCVAY PSGFYKPEGLVOEY
SKRVKYS VFSY KNDDYYLDDGGVLRANOK FVOR FVGETKYPEGGETVOEY
SKRVKYS VFSY KNDDYYLDDGGVLRANOK FVOR FVAR PSGFYKPEGLVOEY
SKRVKYS VFSY KNDDYYLDDGGVLRANOK FVOR FVAR PSGFYKPEGLVOEY
SKRVKYS VFSY KNDDYYLDDGGVLRANOK FVOR FVOR FVAR PSGFYKPEGLVYY FX
DNPNEDDAKATTHR VCRT I GNISGV IN YLNKFSOMETGKNTKGFDP VSELYYTAYRY FK
RLGHVPEYSYLTGS VNEKY QOADAF FY I TDMDD PI RYACOSINVYLGIGOTHNIPDKNL
PGNTNTTGEPVK POA VENDRS I DVVKRMAQ I FOMEGRADOAMTSALAPS PHFLVPGA
GNISAY I AALAYDAHTKOMR PDLEGOQLLTTHWVDVVEGGDYK I PI STNOYWLAAKYG
GROVPAGYDEDKT VNPLASRAYPMTNOEY YNGODTKAKRANDFY I AADAEKWVASLKHAF
SRI VAE I KAAGTGLSSNSAR LETGAVTY QAG FF SGTWRGDL I AY HVDKVTGALT PFWN
ANF PAREQRVI K FANATTLOD TYKRNIGGTALASASAQOI NYLHGDRSQGENV PGKLR
I RSGIMGDI VNSQPLYVGA PNGRL YTTANFTCASA YAAF AAOOANRV PVYVYGANDGM
LHAFDANTGKEI FAF VPRAAMPKLLEYTDONYGHOY YVDGELTAADI Y DTKLGMRSVLL
VGTLGRGGKGLFALDVTD PSNI R LLWDKTSADI GGLGWTLSKPMI AQTSDGTWS VLLG
NGFNSTADNAQLI VNSLLTGHAAOP YNGTSNIGLSGVF PMSSOSING I TDRVYAGDLL
GTLWRFTFSDNÁWKVAPLFTATY QGKAOP I SATPLGALER STGRWH I FRGTGRALSSH
DMDNKENQSWTGLI DOGTTI PGRTRLSGVQI VDEGVVNGYA VRTVSDFKNI GTDGWYM
DLI SPKSGKOGERM I VSIMFRGAALI GTTRI DDNSDI CKLSGGFVMAI NPFTGGRALG
DLI SPKSGKOGERM I VSIMFRGAALI GTTRI DDNSDI CKLSGGFVMAI NPFTGGRALG
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hgggdvpgnlaivasiefftvisvanladtytpgvryvgyfdsnkcykyhyssreldr
yfyfvasprpqanygcnttggvmagnflnmaatqtidffrsaltggyrvadtanetil
                                           complement (4427.
                                                                                               GLNINRVSWREILRP"
                                                                                                                                  <u>QWFFDLNTGGGSGGALNGNPVSGVGVSSAPNSPVFTGNIMQIGADDGTVTSLKTPSSG</u>
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/protein_id="AAO28377.1"
/db_xref="GI:28056498"
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/locus_tag="PD0503"
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|mol_type="genomic_DNA"
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note="identified by
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'note="Pierce's disease
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Paulo, SP 05508-900,
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     RLDYAQNRKSLTTAYQIPAFKWLDGWYIFSARAYDEQTQYIDLRNVKLSAARSGQINR
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Score 20.2; DB 2; Pred. No. 2.5e+02; D; Mismatches 3;

Indels

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Gaps

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HTG 13-JUL-2000 LOW-PASS

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Sequence split into 18
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LMFLCHR34_10

LMFLCHR34_11

LMFLCHR34_12

LMFLCHR34_13

LMFLCHR34_13

LMFLCHR34_15

LMFLCHR34_16

LMFLCHR34_16

LMFLCHR34_17

IMPLCHR34_17
                                                                                                                                                                     Fragment Name
LMFLCHR34 00
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LMFLCHR34 02
LMFLCHR34 03
LMFLCHR34 04
LMFLCHR34 05
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                            18)
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VLLRGGASAFGSKSNFTQLHQQLRWFHGLGSSSRLILRGEVGTTWASDLVAMPPSLRF
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SAFNRYPDWHTGIGIGLRYRSPVGPVRVDIARGLNKPDSKIQLYIDIGANL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-JUL-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K
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Birren,B., Linton,L., Nusbaum,C. and Lander,B.
Mus musculus chromosome 18, clone RP22-32I23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inpublished
                                                                                                                                                                                                                                                                      NOTE: This record contains 81 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 68974)
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L5920
Center clone name: 32_I_23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR Web site: http://www-seq.wi.mit.edu
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Muzny,D., Ansari-Lari,M.A., Timms,K.M., Yu,W., Dugan,S., Lu,J.,
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Direct Submission
Submitted (15-UUL-1997) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Sequencing is completed to a minimum standard of double strand
coverage with a minimum of 2 clones and 2 reads with no ambiguities
or 2 chemistries with a minimum of 2 clones and 3 reads with no
ambiguities. If the sequence quality does not meet this standard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley,K., Chen,B., Forcum,J., Arenson,A.D., Chiu,M.W., Gorrell,J.H., Brundage,B., Di,W., Chinault,C., Nelson,D.
                                                                                                                                                                                                                                                                     Cross-species sequence comparison of the IDS region Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibbs, R.A.
it will be indicated in the annotation.
                                                                                                                                                                                                                       Chiu, M. W.
                                                                                                                                                                                                                                                                                                                             and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                          Timms, K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 110079) mms, K.M., Huckett, L.,
                                                                                                                                                                                                                                           (bases 1 to 110079)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
                                                                                                                                                                                                                                                                                                                                                    Edwards, F.J.,
                                                                                                                                                                                                                                                                                                                                                    Lu,J.,
                                                                                                                                                                                                                                                                                                                                                       Muzny, D.M.,
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                                                                                                                                                                                                                                                                                                                                                          Miller, W.
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The repeat regions shown were identified using Adrian Smit. RepeatMasker by

Sequence similarities were identified using Powerblast by Jinghui

source Exon/Intron boundaries of identified were canonical splice junctions that across the splice junctions.

Location/Qualifiers genes were maintained chosen if there sequence continu continuity

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                                                                                                                                                                                                                                                                                  complement (10633 ...10861)
/rpt_family="LTR/Malk"
complement (10892 ...11185)
/rpt_family="SINE/B4"
complement (11193 ...11366)
/rpt_family="LTR/Malk"
11629 ...1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="LINE,
complement(5257.
/rpt_family="SINE,
6904...6953
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complement(2864. .3101)
/rpt_family="LTR/Retroviral"
                                  /rpt_family="Low_complexity"
complement(12276, .12396)
                                                                                                                                                      /rpt_family="Simple_repeat"
complement(11839..11971)
/rpt_family="SINE/84"
                                                                                                                        complement (12138.
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complement(10494...10582)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/chromosome="X"
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mol_type="genomic DNA"
_family="SINE/B2"
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family="Simple_rep_
- [4982, .5064]
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lement(7980. .8199)
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/rpt_family="scRNAcomplement(21684.
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/rpt_f.
29292.
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complement(23849. .23940)
/rpt_family="SINE/Alu"
25152. .25220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt family="Other/MER21 gro" complement (21582. .21661) /rpt family="Simple_repeat" complement (21662. .21761)
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complement(14783..14914)
/rpt_family="Simple_repeat"
17009..17084
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complement(31179. .31235)
rpt_family="Simple_repeat"
1326
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complement(26165, .263)
/rpt_family="SINE/B2"
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21812
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complement(19902.
      /rpt family="Simple_repeat"
complement(35493. .35633)
/rpt_family="LINE/L1"
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27322.
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                                                     /rpt family="Simple repeat"
complement(34591, .34664)
/rpt family="DNA/MER1_type"
complement(34824, .34916)
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31705.
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14096. .14220
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|oin[14201. .14287,15145. .15281,15929. .16106,17952. .18040,
|8934___19134,20646. .20816,25808. .25934,27982. .28155)
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t family="SINE/MIR"
plement (18187. .18314)
t_family="SINE/Alu"
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family="SINE/B2"
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                                                                                                                                                                                                                                                                                                                                                        family-"SINE/B2"
lement (27695. .27734)
family-"Low_complexity"
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ement(1782)
                                                                                                                                 family="Low_complexity"
                                                                                                                                                                   _family="LINE/L1"
                                                                                                                                                                                              family="Simple_repeat"
                                                                                                                                                                                                                            family="Simple_repeat"
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ement(26370
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_family="SINE/ID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="scRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                         ly="SINE/B2"
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2 (bases 1 to 163132)
Birren,B., Linton,L., Nusbaum,C., Lander,B., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Anderson,S., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Paro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 163132)
Birren,B., Nusbaum,C. and Lander,E.
Musbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                             AC121312 163132 bp DNA Mus musculus clone RP24-343J5, WORKING
                                                                                                                   Unpublished
                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                 AC121312.3 GI:28975922
HTG; HTGS_PHASE1; HTGS_DRAFT.
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/rpt family="LINE/L1"
complement (4069. .40779)
/rpt family="SINE/Alu"
complement (41671. .42216)
/rpt family="LTR/MalR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="SINE/Alu"
43947. .44060
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/rpt family="Simple_repeat"
42539. .42710
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complement(43056. .43106)
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complement(39309...39438)
/rpt_family="SINE/Alu"
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/rpt_family="SINE/B2"
complement (36381. .36489)
/rpt_family="LTR/MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (38986.
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79.3%;
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Pred. No. 5.9e+02;
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CE 3 (bases 1 to 163132)

RS Birren,B., Nusbaum,C., Lander,B., Abulen,N., Ballen,N., Balren,B., Nusbaum,C., Lander,B., Barna,N., Bastien,V., Bloom,T., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Anderson,S., Cook,A., Cooke,P., Corum,B., DeArellano,K., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Lidey,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Lidey,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Lui,A., Mabbitt,R., MacLean,C., MacCian,C., MacCian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 17, 2003 this sequence version replaced gi:25956378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                   NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 160194 bases at least Q40 Consensus quality: 161479 bases at least Q30 Consensus quality: 161963 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert sizė: 168000; agarose-fp
Insert size: 162212; sum-of-contigs
Quality coverage: 8.4 in Q20 bases;
Quality coverage: 8.7 in Q20 bases;
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be updated with the finished sequence
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COMMENT

JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

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135188 CCTGCCCAGGGGTAGCACTTCCTGCAGGG 135216
        AC117138.5 GI:25073145
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                         2 CCTGCGTAGTGGTACGACCTCCTGCAGGG 30
                                                                                          AC117138 176222 bp DNA linear HTG 19-N
Rattus norvegicus clone CH230-385L3, WORKING DRAFT SEQUENCE,
                                                                 unordered pieces.
AC117138
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/db xref="taxon:10090"
/clone="RP24-343J5"
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of 2155 bp
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of 15725 bp
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of 14263 bp
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REFERENCE AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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Cardenas, V., Carter, K., Cowaros, T., Ceaser, H., Center, S., Cardenas, V., Carter, K., Cowaros, T., Ceaser, H., Center, S., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Deraper, H., Dugan-Rocha, S., Dunn, A., Dublin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Falley, M., Falgs, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Guevara, M., Gebregoergis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Gurartne, P., Haeland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderzon, N., Hornendez, J., Harvey, Y., Havlak, P., Hawes, A., Henderzon, N., Hornendez, J., Gackon, L., Jang, H., Johnson, R., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kally, S., Ka
                      Submitted (19.NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23813077.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bem.tmc.edu/projecte/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Ben
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C.
Direct Submission
    individual sequence contigs are ordered and oriented,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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arie., Metzker, M.Lee., Abramzon, S., Adams, C., Aluer, V.,
Allen, H., Alabrooks, S., Amin, A., Angulano, D.,
Allen, H., Alabrooks, S., Baden, H.,
hi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
hi, V., Aoyagi, A., Barber, M., Barnstead, M., Benahmed, F.,
    and separated
                                                                                                                                                                         BASE COUNT
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TITLE JOURNAL REFERENCE

JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

64.7%; 79.3%;

Score 19.4; DB 2; Pred. No. 6.1e+02;

Length 176222;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
end_sequence:BZ134038"
50120 a 34724 c 34881 g 49698 t
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Center clone name: CH230-385L3
Consensus quality: 163801 bases at least Q30
Consensus quality: 166225 bases at least Q30
Consensus quality: 167951 bases at least Q20
Batimated insert size: 166810; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.
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clone_end:T7"
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|mol_type="genomic DNA"
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3316: gap of unknown length
14915: contig of 11599 bp in length
15015: gap of unknown length
139403: contig of 124388 bp in length
139503: gap of unknown length
176222: contig of 36719 bp in length.
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        6799 others
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| FEATURES source repeat repeat repeat repeat | COMMENT | TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL | AC002406 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS | Matches 2 Qy 1 Db 155910 RESULT 10 |
|---|---|--|--|---|
| Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions. Location/Qualifiers 1. 194985 /organism="Mus musculus" /mol type="genomic DNA" /db xref="taxon:10090" /chromosome="x" /clone="B178A13" /rpt family="MSTD" /rpt family="MSTD" /rpt family="G561. 1868) /rpt family="B1AM" /rpt family="B4A" | Baylor Plaza, Houston, TX 77030, USA On Mar 23, 1998 this sequence version replaced gi:2909685. Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation. The repeat regions shown were identified using RepeatMasker by Adrian Smit. Sequence similarities were identified using Powerblast by Jinghui Shang. | Garcia, C., Goodman, M., Gorrell, J.H., Haywood, M., Jackson, L., Jin, S., Kampal, R., Karpathy, S., Leal, B., Li, Y., Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L., Rashid, N.D., Rowland, K., Savage, L., Scherer, S.S., Shen, H., Timms, K.M., Todd, J., Vo, Q., Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A. Direct Submission Unpublished 2 (bases 1 to 194985) Chiu, M.W. Direct Submission Submitted (11-AUG-1997) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 194985) Worley, K.C. Direct Submission Submitted (21-MAR-1998) Human Genome Sequencing Center, Department Submitted (21-MAR-1998) Human Genome Sequencing Center, One | ACO02406 ACO02406 ACO02406 Mouse chromosome X BAC B178A13 (Research Genetics mouse BAC library) complete sequence. ACO02406 ACO02406.1 G1:2981248 HTG. Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (bordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 194985) Muzny, D., Arenson, A.D., Brundage, E., Carvelli, K., Chen, E., Chen, J., Did W Ding V Thoran S Durbin J Forent J Graceb E., Chen, J., | 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0; 1 CCCTGCGTAGTGGTACGACCTCCTGCAGG 29 |
| repeat_region | repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region | repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region | | repeat_region repeat_region repeat_region repeat_region |
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/rpt_family="(CAG)n"
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complement(40951...
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                                                                    Score 19.4; DB 10;
Pred. No. 6.2e+02;
0; Mismatches 6;
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RESULT 11
AL672026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-SBP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 11, 2002 this sequence version replaced gi:21955546.
                                                                                                                                                                         Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-403011 is
from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VECTOR: pBACe3.6.
CACTGCCTAGTGGCATGTCATCCTGCAGG 10107
                                                             CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
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                                                                                                                                                                64.7%;
nilarity 79.3%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP23-403011"
/clone_lib="RPCI-23"
a 44414 c 44985 g 55003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                         0
                                                                                                                                                                                                               Score 19.4;
Pred. No. 6.
                                                                                                                                                      ed. No. 6.2e+02;
Mismatches 6
                                                                                                                                                                                                                                                                   DB 10;
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DNA linear HTG 10-MAY-2003 WORKING DRAFT SEQUENCE, 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allen, C., Allen, H., Alsbrooks, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebehi, V., Avyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Caderon, E., Chu, J., Claecko, J., Chavez, D., Chen, C., Coyle, M., Chen, Y., Chen, Z., Chu, J., Clardenas, V., Carter, K., Cavazos, I., Ceasar, H., Chen, Y., Chen, Z., Chu, J., Clayed, M., Buryant, N., Buhay, C., Burch, P., Burrell, K., Caderon, E., Charle, M., Duyan, R., Chen, Y., Chen, Z., Chu, J., Chen, J.,
         Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:23264219.
The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                     Submitted (07-JUL-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                      3 (bases 1 to 217622)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
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                                                                                                                                                                       Direct Submission
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                                                                                                 RESULT 13
AC113777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                            DEFINITION
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                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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: 222869 bp DNA linear HTG 19-N
Rattus norvegicus clohe CH230-92I15, WORKING DRAFT SEQUENCE,
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                 23;
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and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may sized gaps filled with Ns to the estimated size and be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
----- Genome Center
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35611 CCAGAGTGGTTGTACCAGCTCCTGCAGGG 35639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.h
NOTE: This is a "working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                CCTGCGTAGTGGTACGACCTCCTGCAGGG 30
                                                                                                                                                                                                                           end_sequence:BH335677"
64155 a 44781 c 42696 g 59570 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: GGQP

Center clone name: CH230-27C5

Center clone name: CH230-27C5

Center clone name: CH230-27C5

Assembly program: Atlas 3.0;

Consensus quality: 208914 bases at least Q40

Consensus quality: 210147 bases at least Q30

Consensus quality: 210143 bases at least Q20

Estimated insert size: 218383; sum-of-contigs estimation quality coverage: 7x in Q20 bases; sum-of-contigs estimat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215375
215475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- Project Information
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                 /note="clone_boundary
clone_end:T7
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                         end_sequence:BH335678"
173652. .174206
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mol_type="genomic DNA"
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                                                                                                                        64.7%;
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                                                                                                                           Score 19.4; DB 2
Pred. No. 6.2e+02
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HTG 19-NOV-2002

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                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                    TITLE
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AC113777.5
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 19, 2002 this sequence version replaced gi:23269985.
                                                                                                                                                                                                                                                                                                                                                  Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 222869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D. Anyalebechi, V., Aoyadi, A., Ayodeji, M., Baca, E., Baden, Anyalebechi, M., Baca, E., Baden, B., 
                                                                                                                                                                                                                                                                                       Rat Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: GSGF
Center clone name: CH230-92115
Center clone name: CH230-92115
Center clone name: CH230-92115
Center Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 217955 bases at least Q40
Consensus quality: 218938 bases at least Q30
Consensus quality: 2189754 bases at least Q20
Consensus quality: 219754 bases at least Q20
Estimated insert size: 223449; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.hgsc.bcm.tmc.edu/
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source be preserved. 113341 113441 203689 203789 /mol_type="genomic v... /db xref="taxon:10116" /clone="CH230-92115" 113441. .115233 organism="Rattus norvegicus" /mol_type="genomic DNA" ocation/Qualifiers 113340: contig of 113340 bp in length 113440: gap of unknown length 203688: contig of 90248 bp in length 203788: gap of unknown length 222869: contig of 19081 bp in length.

misc_feature

/note="wgs_contig" 48726 c 48850 g

g 63215 t

2472 others

Matches Query Match Best Local Similarity 47915 CTCTGAGTTCTGGGAGGACCTCCTGCAGG 47943 23; CCCTGCGTAGTGGTACGACCTCCTGCAGG Conservative 64.7**%**; 79.3**%**; 0; Score 19.4; Pred. No. 6 Mismatches 29 .2e+02 DB 2; Length 222869;

ACCESSION VERSION KEYWORDS DEFINITION BX294168/c ORGANISM Mus musculus chromosome X clone RP23-29M4, PROGRESS ***, 5 unordered pieces. BX294168

BX294168 3 GI:31335441

HTG: HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Mus musculus (house mouse) BX294168 226382 bp DNA chromosome X clone RP23-29M4, 5 unordered pieces. linear HTG 02-JUN-2003
*** SEQUENCING IN

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FEATURES
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 224670 bases at least Q40
Consensus quality: 225372 bases at least Q30
Consensus quality: 225812 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-MAY-2003) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 226382)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 225982; sum-of-contigs
Insert size: 202428; 8.8% error; agarose-fp
Quality coverage: 6.28x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: bM29M4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Wellcome Trust Sanger Institute
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humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
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41518
97940
98040
119005
119105
119105
                                                                     fragment_chain: 163669. .226382
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iragment_chain:2
                                                                                                                                             /note="assembly_fragment:00715
fragment_chain:1"
119105. .163568
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                                                                                                                                                                                                                                            fragment_
                                                                                                                                                                                                                                               /note="assembly_fragment:01793
fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-23"
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/chromosome="X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="RP23-29M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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97959: contig of 56422 bp in
98039: gap of 100 bp
119004: contig of 20965 bp in
119104: gap of 100 bp
163568: contig of 44464 bp in
163668: gap of 100 bp
226382: contig of 62714 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baldwin, D., Bandarranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bhahy, C., Burch, P., Burrell, K., Calderon, B., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Checkas, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davy-Carroll, L., De, Anda, C., Dederich, D., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Bgan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Harlak, P., Haldun, S.L., Hodgson, A., Hogues, M., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Jackson, L., Jackson, L., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kovats, C., Kartt, C.L., Lebow, H., Levan, J., Levis, L., Li, Z., Liu, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lous, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Magua, P., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Mangum, A., Mangum, B., Mangum, P., Montemavor, J., Montemavor
Milosavijevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Mankeryis, C., Neal, D., Newton, N., Myuyen, N., Norris, S., Nankeryis, C., Neal, D., Newton, N., Myuyen, N., Norris, S., Nankeryis, C., Neal, D., Newton, N., Myuyen, N., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Reeves, K., Regier, M.A., Reigh, R., Reeves, K., Regier, M.A., Reigh, R., Reeves, K., Reigher, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, M., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Trajos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Maldron, L., Walker, B., Wang, J., Wang, S., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Weiczyk, R., Wooden, H., Worley, K., Williams, G., Willson, R., Weczyk, R., Wooden, H., Worley, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3618 CACTGCCTAGTGGCATGTCATCCTGCAGG 3590
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Allen, C., Allen, H., Alsbrooks. S., Amin. A. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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On May 13, 2003 this sequence version replaced gi:23664762.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: CH230-30II0
Center clone name: CH230-30II0
Center clone name: CH230-30II0
Center Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 215722 bases at least Q40
Consensus quality: 217391 bases at least Q20
Consensus quality: 217391 bases at least Q20
Consensus quality: 218686 bases at least Q20
Batimated insert size: 228373; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                 /note="wgs_end_extension
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5387. ..6218
/note="clone boundary clone end:Sp6 site:EcoRI
                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                      clone="CH230-30I10"
                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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Best Local Similarity
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25155 CTCTGAGTTCTGGGAGGACCTCCTGCAGG 25183
                                                 23;
               1 CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
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clone_end:T7"
a 46853 c 47994 g 64681 t
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224248. .225665
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171226. .217374
/note="clone_boundary
                                                            64.7%;
79.3%;
                                                 0
                                                            Score 19.4;
Pred. No. 6
                                                 Mismatches
                                                            .2e+02
                                                                         DB 2;
                                                                                                              7486 others
                                                                       Length 226790;
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                                                 0; Gaps
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Search completed: September 16, 2003, 19:14:18 Job time: 662.921 secs

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Match Length
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| Naka Tate WPI; | (KYOW | 16-1 07- <i>1</i> 03- <i>1</i> | 18-1 | 20- | EP1 | Cory | cory | C 91 | 26-8 | AAH | RESULT 1 AAH67112/c ID AAH6711: XX | | 45 | 443 | 42 | 410 | 39 | 37 38 | 36 | υ ω : - Α : n | 3 3 3 2 | 31 | 29 | 27 | 2 6 6 | 24 | 2 22 | 21 | 19 | 17 18 | 16 | 15 | 13 | 12 | 110 | 9 |
| gawa S, ishi N, 2001-3 | OW) KYOWA | DEC-1999 APR-2000 AUG-2000 | DEC-2000 | -JUN-2001 | EP1108790-A2 | Corynebacterium | Coryneform borganic acid | glutamicum | SEP-2001 | AAH67112; | 2 st | | 17.4 | 17.4 | 17.4 | 17.4 | • | 17.4 17.4 | 7 | 1 7 | 17.4 17.4 | 7 : | | ٦.٦ | 7. | 17.6 | ٦,٦ | 7. | 7. | | 7 | 7. | . 80 | ω. | о <u>с</u> о | 18.4 |
| Mizogu Senoh 76931/40 | WA НАККО | 20 | ; 2000EP- | • | 2. | | bacterium; d synthesis | m coding | (fir | | andard | | 58.0 | | • | | • | 58.0 | | | | | | • | | | • | 59.3 | • | | | • | • | | 61.3 | 61.3 |
| A, | ско косуо | 99JP-0377484. 00JP-0159162. 00JP-0280988. |)EP-0127688 | | | glutamicum. | ium; am | .ng sequence | irst entry) | | ; DNA; | | | | _ | ~ ~ | | 1062 1196 | | | ~ ~ | ٠ | | | 243 | | 553 | 205 | 035 | 766 035 | 035 | | 503900 | ŏï | 503841 | -, |
| H, Ando Ikeda M, | o XX. | 484. 162. 988. | 688. | | | um. | amino a | ence | Z | | 576 BP | | 23 | 24 | 22 | 222 | 21 | 24 23 | 24 | 2 2 | 2 2 4 2 | 21 | 22 | 3 2 | 23 | 22 8 | 223 | 234 | 24 | 21 15 | 22 | 2 2 | 22 | 22 | 2 22 | 24 |
| Ando S, Hayashi M, la M, Ozaki A; | | | | | | | acid synthesis; vi | fragment SEQ ID NO: | | | יט <u>.</u> | ALIGNMENTS | AAS85690 | AAI58571 AAS99892 | AAS29805 | AAS29780 AAI60357 | AAA52649 | ABL90201 AAS85689 | ABS53342 | AAHO8485 | AAS31449 AB066773 | AAK81679 AAC10137 | AAK78458 | AAK65857 | AAK85946 AAS85688 | ABL19365 | ABL10891 ABY08797 | ABL29461 | ABL62374 | AAA26299 AAO66537 | AAF26352 | ABX82153 ABI:72764 | AAK96733 | AAK95240 | ABTOOOLO | ABA96147 |
| Ochiai K, | | | | | | | vitamin; saccharide | 0: 2147. | | | | | DNA | Human Polyn | Human | Human | Eost | Human DNA er | Corn e | Human | Human Human | Human Human | Human | Huma | Human DNA e | Drog | Drog | Drog | Col | Huma | יסי | Corn | Hur | Hu | Hur | Modi |
| Yokoi H; | | | | | | | ride; | | | | | | encoding novel | polynucie ncleotide | cytoskeleta | cytoskeleta polymucleot | ophil activa | gg | event MO | Ť | cDNA en | | | | encoding novel | Drosophila melanog | Drosophila melanog | Drosophila melanog | on adenocarcino | n secreted pro | | 7 (0 | an neuregulin- | Human neuregulin-1 | uregulin | ed human/mou |

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                Davie
                                                                                                                                                   27-OCT-1995;
                                                                                                                                                                                                                                                                                                EP770678-A2
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29-JUL-1997
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                                                                                                                                                      9508-0005965.
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                                                                                                                                                                                                                                                                                                                                                /note= "the mature protein is encoded by
61-1365 when the AP is expressed
coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                             LIFE SCI INC.
PHARMACIA BIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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90.9%;
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Pred. No. 1.
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E. coli"
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ID AAT66461 standard; DNA; 2936
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Best Local S
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A genomic DNA sequence (AAT66461) from Rhodothermus marinus (Rma) contains the gene for a thermophilic alkaline phosphatase (AP) and flanking regions. It was obtd. by transforming E. coli XL2-Blue MRP' cells with Rma genomic DNA fragments, screening for AP activity on plates contg. a chromogenic indicator, and KpnI digestion of isolated clone pBRM1. A 1.8 kb fragment of pBRM1/KpnI was subcloned into pUCl3 to to yield plasmid pCRM1.8 (AAT66462), and a presumptive full-length coding sequence (AAT66463) for Rma AP (AAM17830) was produced. The Rma AP nucleic acids can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A genomic DNA sequence (AAT66463) from Rhodothermus marinus (Rma) codes for a thermophilic alkaline phosphatase (AP) (AAW17830) that shows optimal activity at pH 10.8 and which is stable to heating at 65 deg for 1 hr. The sequence was deduced from a clone isolated following expression screening of E. coli cells transformed with Rma genomic DNA (see also AAT66461). The Rma AP gene can be used to produce recombinant AP in transformed host cells for use in nucleic acid and protein detection assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable Rhodothermus marinus alkaline phosphatase - useful as enzyme label in immunoassays and nucleic acid assays
                                                                                                                                                                    enzyme
                                                                                                                                                                                                                                            Davis
                                                                                                                                                                                                                                                                                                                27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                          24-OCT-1996;
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29-JUL-1997
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                                                                                                                                                                                    Thermostable
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AMERSHAM PHARMACIA BIOTECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphatase; thermophilic enzyme;
                                                                                                                                         Fig 7; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGTGCGTACTGCTTCGGCCTCCAGCCGGG
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                                                                                                                                                                      Rhodothermus marinus alkaline phosphatase in immunoassays and nucleic acid assays
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(first entry)
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RESULT 4
AAT664622/c
ID AAT66462;
XX
AAC AAT66462;
XX
AC AAT66462;
XX
AC AAT66462;
XX
DT 25-MAR-2003 (updated)
DT 29-JUL-1997 (first entry)
DT 29-JUL-1997 (first entry)
DT 29-JUL-1997 (first entry)
XX
KW Alkaline phosphatase; thermophilic
XW plasmid pCRM1.8; ss.
XX
Chimeric Rhodothermus marinus stra
XX
EP770678-A2.
XX
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PN 24-OCT-1996; 96EP-0307692.
XX
PP 24-OCT-1995; 95US-0005965.
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PP 24-OCT-1995; 95US-0005965.
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PR 27-OCT-1995; 95US-0005965.
XX
PR 27-OCT-1996; 96EP-0307692.
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PR 27
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                                                                                                      Query Match
Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                          Plasmid pCRM1.8 (AAT66463) contains a 1.8 kb HindIII/KpnI segment of genomic DNA (see also AAT66461) containing the alkaline phosphatase (AP) and flanking sequences from Rhodothermus marinus (Rma), cloned into pUC19. This recombinant plasmid has been used to produce Rma thermophilic AP in B. coli JM109 transformants. A presumptive full-length coding sequence (AAT66463) for Rma AP (AAW17830) was deduced. The Rma AP nucleic acids can be used for prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prodn. of recombinant AP
detection assays.
(Updated on 25-MAR-2003 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alkaline phosphatase; thermophilic enzyme; label; assay; plasmid pCRM1.8; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2936 BP; 525 A; 1012 C; 880 G; 519 T; 0
                                                                                                                                                                                                               Sequence 4454 BP; 978 A; 1305 C; 1234 G; 937 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMSH ) AMERSHAM LIFE SCI INC. (AMSH ) AMERSHAM PHARMACIA BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1351 CCGTGCGTACTGCTTCGGCCTCCAGCCGGG 1322
  1738
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CCGTGCGTACTGCTTCGGCCTCCAGCCGGG
                                                      CCCTGCGTAGTGGTACGACCTCCTGCAGGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cccreceracrecraceaccrecrecaege 30
                                                                                                                                                                                                                                                                        25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003 to
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodothermus marinus alkaline phosphatase - in immunoassays and nucleic acid assays
                                                                                                                                                                                                                                                                                                                         for use in nucleic acid and protein detection
                                                                                                                             62.7%;
76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.7%;
76.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an alkaline phosphatase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     correct PA field.)
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                                                                                                         0; Mismatches
                                                                                                                                  Score 18.8; DB 18; Pred. No. 1.5e+02;
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain ATCC 43812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
1709
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                                                                                                                                                         Length
                                                                                                                                                                                                                  other;
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                                                                                                            Indels
                                                                                                                                                            4454;
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RESULT 5
AAH68530/c
ID AAH685
                                    RESULT 6
ABN17942
ID ABN1
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Best Local
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                            sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the printed supports.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C glutamicum coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH68530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH68530 standard; DNA;
                                                                                                                                                                                                                                                          Sequence 349980 BP; 86896 A; 98023 C; 80939 G;
                                                                                                                                                                                                                                                                                     European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum
                         24-JUN-2002
                                                                              ABN17942 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000; 2000EP-0127688
                                                                                                                                                 266823
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20; Conserv
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                                                                                                                                               AGTGGTACGACCACCTGCAAGG
                                                                                                                                                                     AGTGGTACGACCTCCTGCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO: 7065; 246pp + Sequence Listing; English.
                                                                                                                                                                                                     Conservative
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mizoguchi H, Ando
Senoh A, Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000JP-0280988.
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                                                                                                                                                                                                               62.7%;
90.9%;
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                                                                              294
                                                                                                                                                                                                       0,
                                                                                                                                                                                                                  Score 18.8; DB 22;
Pred. No. 2.1e+02;
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Ozaki A;
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                                                                                                                                                 266802
                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                               Length 349980;
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                          0 other;
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Human ORFX polynucleotide sequence SEQ ID NO:4361.

Human; open reading frame; ORPX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; chypertension; hyperthyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;

myasthenia gravis;

gene; 88.

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                                                                                                                                                                                                                                                                                    The present invention describes substantially purified human proteins CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 cl nthe specification). ABN15762 to ABN27252 encode the human ORFX CC proteins given in ABP00010 to ABN15705. CRICK proteins are useful for treating or preventing a pathology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a cyphorome associated with ORFX-associated disorder. ORFX proteins are useful for treating a cyphorome associated with ORFX-associated control of cancer, hyperproliferative disorders, cirrhosis of liver, cypsoriasis, benign tumours, keloid, degenerative disorders related to organ cransplantation, cardiovascular diseases, disorders related to organ cransplantation, cardiovascular diseases, disorders related to organ control of the control o
                                                                                       Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-106308/14.
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                                                                                                                                                                                 Sequence 294 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-)
                                                                                                                                                                                                                                                     specification,
                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
  248
                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed iteation, but was obtained in electronic format directly from WIPO
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CTGGGTTGTGGTTCGACATCTCGCAGGG 275
                                            CTGCGTAGTGGTACGACCTCCTGCAGGG 30
                                                                                         Conservative
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                                                                                                                                                                              A; 63 C; 82 G;
                                                                                                            61.3%;
78.6%;
                                                                                       0,
                                                                                                            Score 18.4;
Pred. No. 1.
                                                                                         Mismatches
                                                                                                                                                                              56 T; 2 other;
                                                                                                            .9e+02
                                                                                                                                 DB 24;
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RESULT 7 ABI99918

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RESULT 8
ABA96146
ID ABA9
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to gene sequences (ABI99915-ABI99934) having modified expression in fetal heart tissue as compared to adult heart tissue and the encoded proteins (ABB57375-ABB57392). The genes have cardiant activity and may be useful in the promotion of the repair of damage to heart tissue caused by myocardial necrosis. The gene sequences are useful for screening potential compounds for the ability to influence disease associated with myocardial necrosis. Drugs identified by the screening methods may be used to treat and prevent disease with which myocardial necrosis is associated, such as cardiac hypertrophy and cardiac insufficiency. Diagnosis of diseases such as those above is also is associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for screening caused by myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes having differential expression useful for screening potential drugs caused by myocardial necrosis -
                Chimeric - Homo sapiens.
Chimeric - Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                               Sequence 3653 BP; 845 A; 1090 C; 1048 G; 670 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             disclosed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 84-90; 171pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-2001; 2001WO-JP03700.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac insufficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; heart; cardiant; myocardial necrosis; cardiac hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat mucocardial cell proliferation associated cDNA SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2002
                                                         orthologous
                                                                       Human; mouse;
                                                                                                     Modified
                                                                                                                                15-APR-2002
                                                                                                                                                              ABA96146;
                                                                                                                                                                                           ABA96146 standard; DNA; 4705
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                                                                                                                                                                                                                                                                                                                        Local Similarity
les 22; Conserv
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DB; ABB57378.
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                                                                                                     human/mouse
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                                                          bone marrow transplantation; ds.
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                                                                                                                                (first entry)
                                                                        Bcr-Abl; cancer; cytostatic; immunosuppressive; leukaemia;
                                                                                                                                                                                                                                                                                                                                     61.3%;
78.6%;
                                                                                                     Brc-Abl fusion
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Pred. No. 2.3e
0; Mismatches
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                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in fetal and adult heart tissue for promoting repair of damage
                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                        2.3e+02
                                                                                                      #
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ABA96147 9
ABA96147
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XX Chim
OS Chim
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Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                  Modified human/mouse Brc-Abl fusion gene #2
                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA96147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancers including leukaemia. The invention also supplies a method useful for purging bone marrow to allow for orthologous bone marrow transplantation, and as a therapeutic option for chronic myelogenous
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                      29-JUN-2001; 2001WO-US20602
                                                                  03-JAN-2002.
                                                                                                      WO200200024-A1
                                                                                                                                                                                                                                                                                                                                      Human; mouse; Bcr-Abl; cancer; cytostatic; immunosuppressive; leukaemia;
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| FT intron 8263561034242 FT /*tag= i FT /number= 4 | exon | on | /*tag= /number exon 826010. | intron | /*tag= /number= 244641 | /*tag= /number= intron 244349 | exon | FH Key Location/Qualifiers FT CDS 2443121369465 FT /*tag= 7 | Homo sapiens. | KW Human; neuregulin 1; neuregulin-1-associated gene 1; NRG1; NRG1AG1; KW schizophrenia; chromosome 8p12; single nucleotide polymorphism; SNP; KW neuroleptic; gene therapy; gene; ds. | AX DE Human neuregulin 1 gene. XX | 07-NOV-2 | XX ABT01503; | RESULT 11 ABT01503/c ID ABT01503 standard; DNA; 1503841 BP. | | QY 1 CCCTGCGTAGTGGTACGACCTCCTGCAG 28 | Query Match 61.3%; Score 18.4; DB 24; Length 1503841; Best Local Similarity 78.6%; Pred. No. 3.1e+02; Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0; | /number= | /number= intron 634442 /*tag= | /number= exon 634335 | intron (| FT exon 631283.651320 FT exon 631283 bg | FI intron 631188.631282 FT /*tag= bf | FT exon 630975631187 FT /*tag= be |
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                  This sequence represents the human neuregulin-1 associated gene 1 (NRG1AG1) of the invention. The NRG1AG1 gene is also referred to as the human Schizophrenia gene. The invention also relates to fragments or variants of the gene and the NRG1AG1 polypeptides they encode. The NRG1AG1 nucleic acids and polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NRG1AG1 expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of NRG1AG1 by expressing inactive proteins or to supplement the patients own production of NRG1AG1. Additionally, the gene may be used to produce NRG1AG1 and income that of the patients own production of the patients.
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                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 90-501; 750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for preventing diagnosing and treating schizophrenia -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK95240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neuregulin-1 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.3%;
nilarity 78.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number= 4a
634442.635331
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631321.634334
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; Pred. No. 3.1e.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
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3.1e+02;
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NRGIAG1. Additionally, the gene may be used to produce NRGIAG1 polypeptides, by inserting the nucleic acids into a host cell and

888888888888888

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RESULT 13
AAK96733/c
ID AAK967
XX AAK967
XX AAK967
XX Human
XX Human;
XX Human;
XX WO2001
XX WO2001
XX O7-SEP
XX O7-SEP
XX (DECO-
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Best Local S
Matches 22
This sequence represents the human neuregulin 1 gene of the invention. The invention also relates to fragments or variants of the neuregulin 1 gene. The gene and its proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate neuregulin 1 expression, such as schizophrenia. For example they may be used to treat disorders associated with decreased neuregulin 1 expression by rectifying mutations or deletions in a patient's genome that affect the activity of neuregulin 1 by expressing inactive proteins or to supplement the patients own production of polypeptides. Additionally, the gene may be used to produce the neuregulin 1 protein, by inserting the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            culturing the cell to express the protein. The gene may also be used as DNA probes and primers in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The NRGIAGI polypeptides may also be used as antigens in the production of antibodies against NRGIAGI and in assays to identify modulators of NRGIAGI expression and activity. Anti-NRGIAGI antibodies and antagonists may also be used as diagnostic agents for detecting the presence of NRGIAGI polypeptides in samples. NRGIAGI is associated with schizophrenia which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG67944, AAG67945, AAG67946, AAG67947, AAG67948, AAG67949, AAG67950, AAG67951, AAG67952, AAG67953, AAG67954, AAG67955, AAG67955, AAG67955, AAG67956, AAG67957, AAG67958, AAG67967, AAG67967, AAG67968, AAG67968, AAG67968, AAG67968, AAG67968, AAG67969, AAG67969, AAG67969, AAG67969, AAG67969, AAG67969, AAG67969, AAG67971, AAG67972, AAG67973, AAG67974, AAG67975.
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                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                               preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuregulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stefansson H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; neuregulin 1 gene; schizophrenia; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                     Page 345-756; 756pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acids and proteins useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                        treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steinthorsdottir V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG67939,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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0; Mismatches
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gulcher JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 801341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for diagnosing
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into a host cell and culturing the cell to express the protein. The gene and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The protein may also be used as antigens in the production of antibodies against neuregulin 1 and in assays to identify modulators of neuregulin 1 expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of neuregulin 1 in samples.
Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
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밁 S Best Loc Matches 801368 CCCTGACTAGTGGGAAGACAGCCTGCAG 801341 22; -CCCTGCGTAGTGGTACGACCTCCTGCAG Conservative .. Mismatches 28 9 Indels 0 Gaps

Query Match

Local

Similarity

61.3%;

Score 18.4; Pred. No. 3.

3.1e+02 DB 22;

Length

1503900;

0

용 Ş

corn ear-specific profile; gene transcription; gene expression; hybrid plant; desirable trait expression; plant breeding prograinheritance; desired characteristic; growth; development; Zea mays. multigene .trait; plant; gene; ss. disease resistance; environmental adaptability; quality; SATMON023; structural Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; Corn ear-derived 24-APR-2003 ABX82153; ABX82153 standard; cDNA; 288 (first entry) polynucleotide (cpd) #613 gene; functional gene; regulatory gene; ВÞ yield; program;

05-NOV-2002 US6476212-B1 Lalgudi (INCY-) INCYTE GENOMICS INC 26-MAY-1998; 14-MAY-1999; R۷, Ito LY, 98US-086722P 99US-0313294. Sherman 뫉;

Novel purified corn-ear derived polynucleotide useful as hybridization probe for detecting polynucleotide in sample, and for identifying, evaluating, and altering desired characteristics associated with development

WPI; 2003-208840/20.

Examples; SEQ ID No 613; 390pp; English.

The present invention relates to the isolation of corn ear-derived polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON023 and SATMON023. Some of the cpds uniquely identify structural, functional, and regulatory genes of corn ear. The polynucleotides sequences are useful for detecting cpds in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in inbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cdps are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, nucleic

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RESULT 15
ABL72764/c
ID ABL727
XX ABL727
XX ABL727
XX ABL727
XX ABL727
XX Corn;
XW Corn;
XW inheri
PH Inheri
XW Inhe
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Best Local S
Matches 19
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The present sequence describes a purified corn tassel-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence pellynucleotide sequence (cdps). To ABL76833. The cdps sequences encode corn tassel-derived polypeptides (CDPs). The cdps sequences (I) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable
                                                                                                                                                                                                                                                                                                                                      Novel purified corn tassel-derived polynuclectide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL72764 standard; cDNA; 289 BP
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Search completed: September 16, Job time : 157.297 secs 2003, 18:37:05

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

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US-09-252-991A-6704/c
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RESULT 2
US-09-252-991A-6599
US-09-252-991A-6599
Sequence 6599, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
FILLE OF INVENTION: NUCLERC ACID AND AMINO ACID SEQUENCES RELATING:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO.6599
LENGTH: 510
TYPE: DNA
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6704
LENGTH: 483
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNO:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
ON: AERUGHIOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
                                                                                                                                                                                                                                                                          Rubenfield et al.
NUCLEIC ACID AMINO ACID SEQUENCES RELATING
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79.3%;
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SEQ ID NO 6639
LENGTH: 3084
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6639
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SEQ ID NO 6578
LENGTH: 3273
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Patent No. 655179
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                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR ETITING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                           TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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5. 6551795
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                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCGGCGCAGTGGGGCGAGCGCCTGCAGG 375
                              CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
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                                                               64.7%;
llarity 79.3%;
Conservative
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79.3%;
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79.3%;
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                                                             Score 19.4; D
Pred. No. 13;
0; Mismatches
                                                               0;
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Pred. No. 10;
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Pred. No. 12
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                                                                                              DB 4;
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                                                                                                Length 3273;
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RESULT 6 US-08-738-172-1/c

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Sequence 1, Application US/08738172 Patent No. 5939257

GENERAL INFORMATION:

APPLICANT: Szasz, Joseph APPLICANT: Davis, Maria TITLE OF INVENTION: THE

Joseph

THERMOSTABLE ALKALINE PHOSPHATASES

NUMBER OF SEQUENCES:

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US-08-738-172-3
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                                                                         Matches
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,965
FILING DATE: October 27, 1995
APPLICATION NUMBER: 08/465,003
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/575,354
FILING DATE: December 20, 1995
APPLICATION NUMBER: 08/240,158
FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/229,229
FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/229,329
FILING DATE: APPLICATION:
APPLICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: IBM P.C. SOFTWARE: WOR'D PATFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/FILING DATE:
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
LENGTH: 1368 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Szasz, Joseph
APPLICANT: Davis, Maria
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                         TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                               TOPOLOGY:
197 CCGTGCGTACTGCTTCGGCCTCCAGCCGGG 226
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                      1 CCCTGCGTAGTGGTACGACCTCCTGCAGGG 30
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633 West Fifth
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76.7%;
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                                                                                      Score 18.8;
Pred. No. 21;
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

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RESULT 7
US-08-738-172-2/c
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                                                                                                                                                                                                                                                                    Sequence 2, Application US/08738172 Patent No. 5939257
                                                                                                                                                                ARENT NO. 3777710N:
GENERAL INFORMATION:
APPLICANT: Szasz, Joseph
APPLICANT: Davis, Maria
APPLICANT: Davis, Maria
APPLICANT: Davis, Maria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MRDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: October 27,
                                                                                                                                                              TITLE OF INVENTION: TH NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/240,
FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/229,
FILING DATE: April 18, 1994
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 22:
                                                                                                                ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2936 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/465,003
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/575,354
FILING DATE: December 20, 1995
APPLICATION NUMBER: 08/240,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                              CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                     1351
                                                                                                                                                                                                                                                                                                                                                                                                  1 CCCTGCGTAGTGGTACGACCTCCTGCAGGG 30
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                                                                                 California
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633 West Fifth Street
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er 27, 1995
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Pred. No. 23
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                                                                                                                     ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No.
US-09-313-294A-613
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                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 613
LENGTH: 288
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 613, Application US/09313294A Patent No. 6476212
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                                                  Best Local Similarity
Matches 19; Conservat
                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/575,354
APPLICATION NUMBER: 08/575,354
FILING DATE: December 20, 1995
APPLICATION NUMBER: 08/240,158
FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/229,329
FILING DATE: APPLI 18, 1994
ATTORNEY/ACENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 3,327
REGISTRATION NUMBER: 3,327
                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: WORD Perfect 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 222/158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/005,965 FILING DATE: October 27, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 4454 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1738 CCGTGCGTACTGCTTCGGCCTCCAGCCGGG 1709
10 GTGGTACGACCTCCTGCAGGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCTGCGTAGTGGTACGACCTCCTGCAGGG 30
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                                                    Conservative
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NIMBER: 08/575,354
NIMBER: 20, 1995
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76.7%;
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                                                                  Score 17.8; DB 4; Pred. No. 48;
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Pred. No. 2
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208 GTGGTACGACCTCCGGCTGGG 228

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-904-615-29/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US93-12464-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1743)
OTHER INFORMATION: n equals a,t,g, o
NAME/KEY: SITE
LOCATION: (1748)
OTHER INFORMATION: n equals a,t,g, o
NAME/KEY: SITE
LOCATION: (1749)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6566325
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/097,917
PRIOR TILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 1766
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: The Regents of the University of California, et al. TITLE OF INVENTION: METHOD FOR INHIBITION OF CELL TITLE OF INVENTION: ADHESION TO RECEPTORS CONTAINING SELECTINS
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
                                                                                   FILING DATE:
                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1312 CCCTGCGTGTTGCTTCCCACTCCTGCAGG 1284
                                                                                                                                                                                                                                                90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application PC/TUS9312464
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                                                                               21-DEC-1993
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75.9%;
                                                                                                    PCT/US93/12464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.8;
Pred. No. 59;
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RESULT 11
US-09-453-702B-252/c
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Best Local Similarity 75.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 252, Applicat Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                            INFORMATION FOR SEQ ID NO: 252: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FD.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHAX: (619) 455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: D
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2035 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 252:
                                                                                                                                                                TELECOMMUNICATION INFORMATION
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Blattner, Frederick R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 CCCGGAGGAGTGGGCCGACCTCTTCCAGG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
                                                      LENGTH: 12848
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPHA-L-FUCOSIDASE
                                                                                                                                                                                                                    NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                 TELEFAX:
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                                                                                                                                                 (808)
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                                                                                                                                                 251-9166
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                                                                                                                                                                    251-5000
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Pred. No. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Migmatches
                                                                                                                                                                                                     960296.95017
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Best Local Similarity
Matches 22; Conserva
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US-09-453-702B-137/c
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                                                  RESULT 13
US-09-620-312D-458
                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 137:
US-09-453-702B-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-453-702B-252
Sequence 458, Application US/09620312D Patent No. 6569662 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 137, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                        15720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 53701-2113

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4539 CTTGCTGAGCGGGAAGACCTCGTGCAGGG 4511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                     2 CCTGCGTAGTGGTACGACCTCCTGCAGGG 30
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Similarity 75.9%;
                                                                                                                      CTTGCTGAGCGGGAAGACCTCGTGCAGGG 15692
                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                               LENGTH: 48908
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                        Conservative
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Burland,
Nicole T.
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Plunkett, ve
An Rod
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75.9%;
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Pred. No. 86;
0; Mismatches
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Pred. No. 74;
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SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,005A FILING DATE: 05-UN-1995 CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

08/188,426

COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

STATE:

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CITY: Washington

COMPUTER: IBM CON OPERATING SYSTEM:

IBM Compatible

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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6599662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILLING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/52,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
                                                                                                                                        Sequence 9, Application US/08469005A Patent No. 5665874
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: pt_FL_genes Version 1.0 SEQ ID NO 458
                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-01-21
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                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (271)..(1161)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT: KUHAJDA, FRANCIS P.
APPLICANT: PASTERNACK, GARY A.
TITLE OF INVENTION: CANCER RELATED ANTIGEN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 1520
                                                                                                                                                                                                                                              277 CCGGAGITCTTGTACGACCTGCTGCAG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asundi, v....
Zhang, Jie
Zhang, Jie
Ren, Feiyan
: Chen, Rui-hong
f: Zhao, Qing A.
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Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang, Dunrui
Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                58.0%;
                                                                                                                                                                                                                                                                                                                                Score 17.4;
Pred. No. 87;
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                                                                                                                                                                                                                                                                                                                                               DB 4;
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                                                                                                                                                                                                                                                                                                                                               Length 1520;
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APPLICANT: ELLIS, CATHERINE
APPLICANT: LONSDALE, JOHN
APPLICANT: LONSDALE, JOHN
APPLICANT: MCONEY, JEFFREY L.
APPLICANT: MCONEY, JEFFREY L.
APPLICANT: DEPIERA, MEGAN E.
APPLICANT: DEPIERA, MEGAN E.
APPLICANT: DEPIERA, CONRAD
TITLE OF INVENTION: HUMAN FAS
FILE REFERENCE: GP-70603
CURRENT APPLICATION NUMBER: US/09/261,907A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 8519
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-261-907-1
Search completed: September 16, 2003, 20:42:38 ob time: 40.3168 secs
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; LOCATION: 124...7650
; OTHER INFORMATION:
US-08-469-005A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.3%; Score 17.2; DB 1; Length 8460; Best Local Similarity 73.3%; Pred. No. 1.3e+02; Matches 22; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                           Query Match 57.3%;
Best Local Similarity 73.3%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09261907A Patent No. 6294364
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: POSOCIACH, Laurence H
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 062482-0113
TELECHMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEPHONE: 202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 8460 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: 6ingle
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILLING DATE: 24-JAN-1994
APPLICATION NUMBER: 08/096,908
PILING DATE: 26-JUL-1993
APPLICATION NUMBER: 07/917,716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3550 CCTTGCACAGTTGCAGCTCCTCCTGCAGGG 3521
                                                                                     3582 CCTTGCACAGTTGCAGCTCCTGCAGGG 3553
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                                                                                                                                                                         Score 17.2; DB 3;
Pred. No. 1.3e+02;
0; Mismatches 8;
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                 Score
       seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08 NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10 PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10 PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10 PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10 PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10 PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10 PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10 PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10 PUBCOMB.seq:*
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Gapop 10.0 , Gapext 1.0
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 64.7 110079 14
64.7 110079 14
64.7 9025608 14
62.7 1566 10
62.7 1593 14
62.7 2936 9 U
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Match Length
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 3 14 US-10-156-761-5071
6 9 US-09-191-989-1
4 9 US-09-191-989-2
6 10 US-09-816-095-3
6 10 US-09-816-095-3
6 13 US-10-027-632-39424
6 13 US-10-027-632-59209
                                                                                                                                                                                         14 US-10-156-761-4750

14 US-10-175-523-96

18 14 US-10-156-761-1

10 US-09-738-626-2147

9 US-09-191-989-3

14 US-10-156-761-5071
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Sequence 4750, Ap
Sequence 96, Appli
Sequence 1, Appli
Sequence 2147, Ap
Sequence 3071, Ap
Sequence 5071, Ap
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 52024, A
Sequence 58202, A
Sequence 1, Appli
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Sequence 59209, A
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| 17.4. | 17.4 17.4 | 17.4 17.4 | 17.4 17.4 17.4 | 17.6 17.4 | 17.8 | 17.8 | 17.8 | 17.8 | 17.8 | 17.8 17.8 | 17.8 | 17.8 | 17.8 | 17.8 | 17.8 | 17.8 | 17.8 | 18.4 | 18.4 | 18.4 |
| 58.0 | 58.0 | 58.0 | 58.0 58.0 | 58.7 | 59.3 | 59.3 | 59.3 | 59.3 | . es | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 59.3 | 61.3 | 61.3 | 61.3 |
| 879 1520 | 799 799 | 700 700 | 403 606 700 | 12404 81 | 9025608 | 48908 | 12848 | 2375 | 2162 | 2035 | 1766 | 1766 | 1766 | 1766 | 745 | 630 | 289 | 1503841 | 1503841 | 1503841 |
| 14. | 9 | 13 | 11 10 13 | 10 | 12 | 14 | 14 | 12 | 14 | 12 | 14 | 12 | 9 | 9 | 13 | 14 | ø | 10 | 9 | Q |
| US-09-951-470-4 US-10-037-270-458 | US-09-764-870-263 US-10-125-540-263 | US-10-027-632-150979 US-10-027-632-150980 | US-09-918-995-16763 US-09-951-470-6 US-10-027-632-150978 | US-10-108-605-236 US-09-783-590-7470 | US-10-156-761-1 US-10-021-660-36 | US-10-114-170-137 | US-10-114-170-252 | US-10-205-194-30 | US-10-198-846-13433 | US-09-873-367C-711 US-10-156-761-4847 | US-10-054-988-29 | US-10-055-098-29 | US-09-904-615-29 | US-09-739-254-29 | US-10-027-632-146355 | US-10-156-761-7444 | US-09-294-093B-2138 | | US-09-795-686-1 | US-09-795-668-1 |
| Sequence 4, Appli Sequence 458, App | Sequence 263, App | | Sequence 16763, A Sequence 6, Appli Sequence 150978, | Sequence 236, App Sequence 7470, Ap | 36, | Sequence 137, App | 252 | | 13433 | Sequence 711, App Seguence 4847, Ap | 29, | 29, | | Sequence 29, Appl | Sequence 146355, | Sequence 7444, Ap | 138 | e H | ۲, | Sequence 1, Appli |

ALIGNMENTS

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                                                                                                                                                                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1323)
US-10-156-761-4750
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US-10-156-761-4750
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4750
LENGTH: 1323
TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                              Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4750, Application US/10156761 Publication No. US20030119018A1
    689
                                         CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
CCCCGGAAGCGTACGACGTCCTGCTGG 697
                                                                                     Conservative
                                                                                                       64.7%;
79.3%;
                                                                                   : 0; Mismatches
                                                                                                         Score 19.4;
Pred. No. 2
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Gaps

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; NAME/KEY: misc feature
; LOCATION: (1). (110079)
; OTHER INFORMATION: where n may be a or g or c or t/u, unknown, or other US-10-175-523-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFIMAL
SEQ ID NO 96
PARCITH: 110079
                  NUMBER OF S
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Publication No. US20030119018A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                            FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                   APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS) FILE REFERENCE: 3235/1J795-US3 CURRENT APPLICATION NUMBER: US/10/175,523 CURRENT FILING DATE: 2002-06-18 PRIOR APPLICATION NUMBER: US 60/299,151 PRIOR FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Evans, David
                                                                                                                                                                                                                     APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITILE OP INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 60/349,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/317,828 PRIOR FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/325,150 PRIOR FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brockman, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4399 CACTGCCTAGTGGCATGTCATCCTGCAGG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/361,834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
9025608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palfreyman, Michael
Rajan, Prithi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klimczak, Leszek
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79.3%;
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Pred. No. 26;
0; Mismatches
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Best Local Similarity
Thehes 23; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Corynebacterium glutamicum US-09-738-626-2147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOPTWARE: PatentIn ver.
SEQ ID NO 2147
LENGTH: 576
                                                                                                                                                                                             Sequence 3, Application US/09191989 Patent No. US20020055098A1
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2147, Application US/09738626 Publication No. US20020197605A1
                                                                        GENERAL INFORMATION:
APPLICANT: Szasz, Joseph
APPLICANT: Davis, Maria
TITLE OF INVENTION: THERMOSTABLE ALKALINE PHOSPHATASES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ALDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (4187715)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptomyces avermitilis
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                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                        258 AGTGGTACGACCACCTGCAAGG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             62.71;
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79.3%;
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Pred. No. 23
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.8;
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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90071-2066 READABLE FORM:

U.S.A.

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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JF 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 5071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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FILING DATE: October 25,1970
APPLICATION NUMBER: 08/465,003
APPLICATION NUMBER: 08/575,354
APPLICATION NUMBER: 08/240,158
APPLICATION NUMBER: 08/240,158
FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/229,329
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                       APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA
APPLICANT: IKED
                      LENGTH: 1593
TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (*--)
TELEFAX: 67-3510
TOTEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 CCGTGCGTACTGCTTCGGCCTCCAGCCGGG 226
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1 Similarity 76.7%;
23; Conservative
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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; LOCATION: (1)..(1593)
US-10-156-761-5071
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      Matches
                                  Query Match
Best Local Similarity
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Patent No. US20020055098A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: October 25,1996
APPLICATION NUMBER: 08/465,003
FILLING DATE: June 5, 1995
APPLICATION NUMBER: 08/575,354
FILLING DATE: December 20, 1995
APPLICATION NUMBER: 08/240,158
FILLING DATE: May 10, 1994
APPLICATION NUMBER: 08/229,329
FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/229,329
FILING DATE: May 11, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 32,327
REFERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Szasz, Joseph
APPLICANT: Davis, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                  LENGTH:
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      Conservative
                                                                                                                                                              linear
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76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/738,172
; Score 18.8; D; Pred. No. 50; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOS 5.0
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                                                                 Length 2936;
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   Gaps
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1 CCCTGCGTAGTGGTACGACCTCCTGCAGGG 30

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RESULT 9
US-09-816-095-3/c
US-09-816-095-3/c
; Sequence 3, Application US/09816095
; Patent No. US20020137164A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              문
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US-09-191-989-2/c
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Best Local S
Matches 23
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CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/738,172
APPLICATION NUMBER: 08/465,003
APPLICATION NUMBER: 08/465,003
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/575,354
APPLICATION NUMBER: 08/575,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09191989 Patent No. US20020055098A1
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,989
APPLICANT: GAN, Weiniu
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                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
SEQUENCE HARACTERISTICS:
SEQUENCE HARACTERISTICS:
SEQUENCE HARACTERISTICS
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: December 20, 1995
APPLICATION NUMBER: 08/240,158
FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/229,329
FILING DATE: April 18, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: THERMOSTABLE ALKALINE PHOSPHATASES NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Szasz, Joseph
APPLICANT: Davis, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (21)
TELEFAX: 67-3510
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90071-2066
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                                                                                                                                                                  1738
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                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                        linear
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Pred. No. 4
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RESULT 11
US-10-027-632-39424/c
; Sequence 39424, Application US/10027632
; GENERAL INFORMATION:
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, NAME/KBY: misc_feature

; LOCATION: (1).T. (99916)

; OTHER INFORMATION: n = A,T,C or G

US-09-816-095-3
                                                                                                                                                                                                                                                                          ; ORGANISM: Corynebacterium glutamicum US-09-738-626-1
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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US-09-738-626-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001147
CURRENT APPLICATION NUMBER: US/09/816,095
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FREISEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin ver.
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                    Query Match
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ORGANISM: Human
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                                                                                                                     2066823
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Local Similarity 90.9%; Pred. No. 4
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Local Similarity 76.7%;
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                                                                                                                   1 CCCTGCGTAGTGGTACGACCTCCTGCAGGG 30
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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Pred. No. 48
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58202
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    Best Loc
Matches
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

EIGHT DEFERRED.
                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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TYPE: DNA
ORGANISM: Human
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                           NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-04-20
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                                                                                                                                      D ID NO 58202
LENGTH: 536
                    Local Similarity
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                                                                                                                                                                                                                                                                       FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-03-29
APPLICATION NUMBER: US 60/185,218
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                                                                                                                                                                                                                                                       FILING DATE: 1999-09-28
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    Conservative
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                  61.3%;
78.6%;
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  0
                  Score 18.4;
Pred. No. 7
  Mismatches
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                                      DB 13;
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                                      Length 536;
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  Indels
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US-10-027-632-59209/c
                                                                 PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1990-12-3
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PRILING DATE: 1999-09-28
PRIOR PRILING DATE: 1999-09-28
PRIOR PRILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
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SEQ ID NO 59209
LENGTH: 536
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GENERAL INFORMATION
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 309173
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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CURRENT FILING DATE: 2002-04-30
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22; Conser
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78.6%;
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Pred. No. 76;
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Sequence 1, Application US/10312918
Publication No. US20030162740A1
GENERAL INFORMATION:
APPLICANT: Regents of the University of California
APPLICANT: Wang, Jean Y.J.
APPLICANT: Vigneri, Paolo
TITLE OF INVENTION: New Strategy for Leukemia Therapy
FILE REFERENCE: 6627-PC0159
CURRENT APPLICATION NUMBER: US/10/312,918
CURRENT ELING DATE: 2002-12-27
PRIOR APPLICATION NUMBER: 60/215,595
PRIOR APPLICATION NUMBER: 60/215,595
PRIOR APPLICATION NUMBER: 60/215,595
PRIOR APPLICATION NUMBER: 07-200-06-30
NUMBER OF 580 ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 4705
TYPE: DNA
ORGANISM: Homo sapien/ Mus musculus
                                                                                                                                                                                                                                                                              FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(4704)

OTHER INFORMATION:

US-10-312-918-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 536
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-309173
Search completed: September 16, 2003, 22:54:38 Job time : 131.416 BECB
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US-10-312-918-1
                                                                                                                                                                                 Query Match 61.3%; Score 18.4; DB 12; Length 4705; Best Local Similarity 78.6%; Pred. No. 75; Matches 22; Conservative 0; Mismatches 6; Indels 0;
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                                                                                       117 CTGCGTAATGACACTCCCTCCAGCAGGG 90
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Title:
Perfect score:
Sequence:
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Maximum
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Maximum Match 100%
Listing first 45 sm
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seq length: 2000000000
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                                        %
Query
Match Length
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| 6 BY70 | BY702686 | 4 | 391 | 62.7 | 18.8 | 42. |
| 7096 | HSM090445 | | 366 | 62.7 | 18.8 | w |
| 335529 BY33552 | BY335529 | w | 340 | 62.7 | 18.8 | N |
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| 06374 | BM806374 | 2 | 1105 | 63.3 | 19 | 0 |
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| 52898 | 2 | 29 | 814 | 63.3 | | œ |
| w | CNS03DKF | 29 | 794 | • | 19 | 7 |
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| 52994 EST4454 | BF252994 | 0 | 623 | 63.3 | | u |
| 9480 h | AW469480 | | 568 | 63.3 | 19 | 4 |
| 16405 HS_2262 | AQ216405 | œ | 432 | w | 19 | ω |
| 1816 BB2618 | BB261816 | 0 | 241 | 63.3 | 19 | N |
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| wlsul. | CA666652 | 14 | 555 | 64.0 | 19.2 | 0 |
| wlsul. | CA669616 | 14 | 402 | 64.0 | 19.2 | 9 |
| wlm96. | CA690063 | 14 | 380 | 64.0 | | 8 |
| Mus | AK042427 | H | 2869 | 64.7 | 19.4 | 7 |
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| 75739 nad03-1 | D4757 | 4 | 161 | • | 19.6 | ø |
| 63661 BY46366 | an. | Ļ | 450 | 9 | 19.8 | Φ |
| 327791 6029795 | 277 | N | 723 | | 20 | 7 |
| 6672 v | 667 | 9 | 652 | 66.7 | N | σ, |
| AL296743 Tetraodon | CNS04LYM | 29 | 980 | 68.0 | 20.4 | u |

ALIGNMENTS

| | COMMENT | AUTHORS | REFERENCE | SOURCE ORGANISM | ACCESSION VERSION KEYWORDS | RESULT 1 BG288880 LOCUS DEFINITION |
|---|---|---|--|-----------------------------------|--|--|
| Email: cgapbs-rémail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAN10398 row: 1 column: 06 High quality sequence stop: 718. | Unpublished Contact: Robert Strausberg, Ph.D. | NIH-MGC http://mgc.nci.nih.gov/. Mational Institutes of Health, Mammalian Gene Collection (MGC) | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleóstomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 900) | Homo sapiens (human) Homo sapiens | mRNA sequence. BG288880 BG288880.1 GI:13044162 EST. | BG288880 900 bp mRNA linear EST 21-FEB-2001 602383822F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4512917 5', |

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RESULT 2
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                                                                                                                                                                                                                                                          Nikaido, I., Obato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Obato, N., Salto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H. Nikaido, I., Obato, N., Salto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, Gough, J., Schamond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Varyis, E. D., Kanai, A., Kawaji, H., Lee, Y., Lenhard, B., Lyons, P. A., Waglott, D.R., Maltais, L., Marchiomi, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Waltsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Saski, D., Shibata, K., Shibata, S., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saski, D., Shibata, E., Rogere, J., Birney, E. and Hayashizaki, Y., Sandai, A., Lander, L., L
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   Laboratory for Genome Exploration Research Group, Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                          Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                Contact: Yoshihide Hayashizaki
Laboratory for Genome Explorat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY707129.1 GI:27118302
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/lab host="DH108 (phage-resistant)"
/clone_lib="NIH MGC_93"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI;
/note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
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/db_xref="taxon:9606"
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URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
H., Koya,S., Miyazaki,A., Murata,M., Nakmura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length oDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
                                                  1 CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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                                                                                                                                      Similarity
CCCTGTGGAGTGGGACGAGCTGCTGCAGG
                                                                                                                                                                                                                                                           140
                                                                                                              Conservative
                                                                                                                                                                                                                                                     /clone lib="RIKEN full-length enriched, adult male testis"
/note="Site 1: XhoI, Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="testis"
/dev_stage="adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
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/clone="1700094C23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain="C57BL/6J"
                                                                                                                                         70.0%;
82.8%;
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Pred. No.
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775
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                                                                                                                                            6.4e+02;
                                                                                                                                                                    DB 14;
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BX264906

337 bp

mRNA

linear

EST 27-FEB-2003

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RESULT 4
BM864032
LOCUS
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AUTHORS
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                                                                                                                                                                                                                                                                81
                                                                         mgcm008x116f.b Magnaporthe grisea
grisea cDNA clone mgcm008x116 5',
BM864032
BM864032.2 GI:30391021
                                                                                                                                                                                                                                                                                                                                         24;
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Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Magnaporthe grisea
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
Email: Madeleine Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klopp,C. and Douaire,M.
Construction and primary characterization of chicken normalized multi-tissue cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX264906 AGENAE Gallus gallus multi-tissues normalized and once-subtracted cDNA library (gcal) Gallus gallus cDNA clone gcal0015c.g.13 3prim, mRNA sequence.
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Archosauria; Aves; Neognathae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Herault, F., Le Meuth-Metzinger, V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pTTT3D-pac; tissues: adipose tissue, brain, kidney, liver, multi-tissues, muscle, ovary, testis, bone marrow, caecum, duodenum, embryos, fabricius gland, granulosa, hypothalamus, ileon, jejunum, oviduct, pancreas, skin, spleen, thymus, utero-vaginal gland, pituitary gland, hematopoietic progenitor cells, small follicle. Clone distribution: AGENAB Resource centre. Francois PIUMI, Francois.Piumi.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LEEG), Domaine de Vilvert, 78352,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Jouy-en-Josas cedex, FRANCE"
1 108 c 77 g 79 t
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/tissue_type="multi-tissues"
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/db_xref="taxon:9031"
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lab_host="DH10B"
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Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                       Score 20.4;
Pred. No. 9
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                                                                                                                                                                     516 bp
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CM Uni-Zap XR Library Magnaporthe
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     AUTHORS
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REFERENCE
AUTHORS
sequence.

ON AL296743.

AL296743.1 GI:8035323

I AL296743.1 GI:8035323

OSS; genome survey sequence.

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tatradontoidea; Tetraodontidae; Tetraodon.

Onssilva,C., Bouneau,L., Fisher,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peterson Bidg, MS2132, College Station, TX 77843-213
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, set
[Rect nr hit (April: 22, 2003) sp[P15710] PHO4 NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
On Mar 7, 2002 this
Contact: Ebbole DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 516)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P.,
K. and Dean,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis genome survey sequence PUC-Ori end of cla
119008 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHATE-REPRESSIBLE PHOSPHATE PCR PRimers
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/note="Vector: pBluescriptSX-; Site 1: ECORI; Site 2: XhoI
/note="Tector: pBluescriptSX-; Site 1: CoRI; Site 2: XhoI
/note="Tector: pBluescriptSX-; Site 1: Side of insert.
/note 1: Side of i
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/cell_type="mycelium"
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clone="mgcm008xI16"
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strain="Guy11"
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Unpublished
Contact Marra M/Mouse EST Project
Contact WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 652)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                vx54d07.rl Stratagene mouse macrophage (#937306) Mus musculus ci clone IMAGE:1279021 5' similar to gb:X54156 rnal CELLULAR TUMOR ANTIGEN P53 (HUMAN); gb:X01237 Mouse mRNA for cellular tumour antigen p53 (MOUSE); mRNA sequence.

AA896672
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Betimate of human gene number provided by genome-wide analysis using Tetracion nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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/mol type="genomic DNA"
/db_xref="taxon:99883"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
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National Institutes of Health, Mammalian Gene Collection (MGC)
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This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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//clone lib="SOLR (kanamycin resistant)"
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                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:1279021"
/lab_host="DH10B (T1_phage-resistant)"
/clome_lib="NCI_CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
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                                                                                                                                            /db_xref="taxon:10090"
                                                                                                              /clone="IMAGE:5132624"
                                                                                                                                                                                 strain="FVB/N"
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., L.B., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C. P., Forrest, L.B., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C. P., Forrest, C.B., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Maltais, L., Marchionni, L., McKenzie, L., Miki, M., Frazer, K.S., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Mi, J., Pessole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Secou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wanner, L., Wahlestedt, C., Wang, Y., Walls, C., Walls, C., Wanner, A., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Yang, L., Yang, L., Yang, L., Wankikawa, T., Konno, H., Nakamura, M., Sakaume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashixume, W., Imotani, K., Ishiata, K., Shipata, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, S., Rogers, J., Birney, B. and Hayashizaki, Y., Sasaki, D., Shibata, S., Shipata, C., Sasaki, D., Shibata, Shibata, Shipata, Shibata, Shibata,
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Saeaki,D., Saro,K., Shibate,K., Shizaki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genon Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCCTGCGTAGTGGTACGACCTCCTGCAG 28
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 450)
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a 176 c 211 g 139 t
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details
                                                                                                                   Similarity
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GGAGTGGTTCGACNTCCTGCAGGG 326
                                        GTAGTGGTACGACCTCCTGCAGGG 30
                                                                                                                                                                                                               102
                                                                                            Conservative
                                                                                                                                                                                                               <u>o</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                      /tissue_type="heart"
/dev_stage="10 days neonate"
/clone_lib="RIKEN full-length
heart"
                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       clone="K630144J20"
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REFERENCE AUTHORS ACCESSION VERSION CD475739/c DEFINITION KEYWORDS ORGANISM 1 (bases 1 to 161)
depamphilis.C., Carlson,J., Ma,H., Frohlich,M., Tanksley,S.,
depamphilis.C., Carlson,J., Arrington,J., Zahn,L., Kong,H.,
Leebenn-Mack,J., Field,D., Arrington,J., Zahn,L., Kong,H.,
Druckenmiller,M., Landherr,L., Hu,Y., Ilut,D., Wall,K., Plock
S.Chiorean,S., Albert, V., Doyle,J., Miller,W., Oppenheimer,D.,
Soltis,D., Soltis,P. and Theissen,G.
Generation of ESTs from early flower buds of Nuphar advena Nuphar advena Nuphar advena Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions
Full sequence and original trace file are available from the Plant 208 Mueller Laboratory, Department State University, University Park, Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; stem Magnoliophyta; Nymphaeaceae; CD475739.1 GI:31397007 CD475739 mRNA sequence. nad03-15ms2-e07 Nad03 Nuphar advena cDNA clone nad03-15ms2-e07 Tel: 814 863 6413 Fax: 814 865 9131 Mueller Laboratory Unpublished CD475739 State University Claude dePamphilis or 161 g James Leebens-Mack P of nRNA Biology, A 16802, USA linear ATTN Rm212, EST 04-JUN-2003 Penn

COMMENT

TITLE

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Nunasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ហ
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., II,
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                             Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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BB872020 RIKEN full-length enriched, 16 days neonate male
diencephalon Mus musculus cDNA clone G630034A16 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group,
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//clone | Ib="Nad03"
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/dev_stage="<= 2.5mm"
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/db_xref="taxon:77108"
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RESULT 11
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 406)
1 (bases 1 to 406)
1 (bases 1, Lacy, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                     Unpublished
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
Washington University School of MedicineP
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vv34a05.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:1224272 5', mRNA sequence.
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RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                     FMAX: 314 200 2002
Email: mouseesr@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
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                    Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 401.
                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
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AA709478.1 GI:2719396
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Location/Qualifiers
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/dev stage="16 days neonate"
/clome lib="RIKEN full-length
male diencephalon"
97 c 129 g 103 t
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/clone="G630034A16"
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/strain="C57BL/6J"
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79.3%;
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                                                                                                             Nikaido, I., Osato, N., Saito, R., Suuki, H., Yamanaka, I., Kyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., LE., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, Bl.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, I., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Hayashizaki, Y., Lander, L., Analysis, of the mouse transcriptome based on functional anotation
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                                              Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
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/mol_type="mRNA"
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23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Nhumazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                    Rattus norvegicus
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                                                                                                                                                                      CB790399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues. Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor,MI 48109-0638 USA)
                                                                                 Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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/dev_stage="12.5 days embryo"
/clone_lib="RIKEN full-length enriched, 12.5 days embryo
Rathke's pouches"
a 100 c 84 g 134 t
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/mol_type="mRNA"
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                                                 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB857961 RIKEN full-length enriched, B16 F10Y cells CDNA clone G370047P05 5', mRNA sequence.
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Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 474)
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/mol_type="mkNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 531)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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further details.
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Site_2: SalI; transgenic moo
                                                                                                                       /organism="Mus musculus"
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/strain="CZECH II"
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| Search completed: September 16, 2003, 20:39:57 Job time : 1522.42 secs | Qy 1 CCCTGCGTAGTGGTACGACCTCCTGCAGG 29 | Query Match 64.7%; Score 19.4; DB 10; Length 531; Best Local Similarity 79.3%; Pred. No. 2.4e+03; Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0; | MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" BASE COUNT 66 a 184 c 169 g 112 t |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| No. | Score | Match | | 8 | ID | Description |
| _ | 20 | 20 100.0 | 20 | 25 | 25 US-09-594-065-1 | Sequence 1, Appli |
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RESULT 1
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                                                                                                                                                         Sequence 1, Application US/09594065

GENERAL INFORMATION:
APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and Kits for Herpes Simplex Virus
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
                                             Matches
                                                            Query Match
Best Local !
                                                                                                                                 ORGANISM: Artificial Sequence PEATURE:
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US-09-821-837-9580
US-09-821-837-9581
                                                            Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                              Mismatches
                                                          2.7e+02;
                                                                           DB 25;
                                                                        Length 20;
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    CURRENT APPLICATION
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US-09-594-065-8

Sequence 8, Application US/09594065

GENERAL INFORMATION:

APPLICANT: WalkerPeach, Cindy
APPLICANT: WalkerPeach, Cindy
ITILE OF INVENTION: Compositions, methods and Kit
TITLE OF INVENTION: Compositions, methods and Kit
TITLE OF INVENTION: Mucheic Acid Detection
FILE REFERENCE: 25436/1280

CURRENT APPLICATION NUMBER: US/09/594,065

CURRENT APPLICATION NUMBER: US/09/594,065

CURRENT FILING DATE: 2000-06-14

NUMBER OF SEQ ID NOS: 14

SOPTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 74

TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WalkerPeach, Cindy
APPLICANT: Dubois, Dwight
TITLE OF INVENTION: Compositions, methods and Ki
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
SOPTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 109
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Best Local Similarity 100.
                                            Sequence 13, Application US/09594065
GENERAL INFORMATION:
APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
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TITLE OF INVENTION: Compositions, methods and TITLE OF INVENTION: Nucleic Acid Detection FILE REFERENCE: 25436/1280
                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
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NUMBER: US/09/594,065

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US-09-594-065-14
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NUMBER OF SEQ ID NOS: 14
SOPTWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 109
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-594-065-14
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                                                                                                  NUMBER OF SEQ ID NOS: 9928
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9580
LENGTH: 481
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Compositions, methods and Kits for Herpes Simplex Virus Type 1 ar TITLE OF INVENTION: Nucleic Acid Detection

FILE REFERENCE: 25436/1280

CURRENT APPLICATION NUMBER: US/09/594,065

CURRENT FILING DATE: 2000-06-14

NUMBER OF SEQ ID NOS: 14

SOPTWARE: PatentIn version 3.0

SEQ ID NO 14

LENGTH: 109
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Best Local Similarity
                                                                                                                                                                                    APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: HOVEL NUCLESIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2076-001
CURRENT APPLICATION NUMBER: US/09/821,837
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/193,481
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WalkerPeach, Cindy APPLICANT: DuBois, Dwight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
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NAME/KEY: misc_feature
LOCATION: (1)...(481)
OTHER INFORMATION: n = A,T,C or G
                                                                                ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%;
l Similarity 100.0%;
20; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Conservative
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Pred. No. 2.
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Pred. No. 2.7e+02;
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Sequence 9581, Application US/09821837
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2076-001
CURRENT APPLICATION NUMBER: US/09/821,837
CURRENT APPLICATION NUMBER: US/09/821,837
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US/09/821,837
PRIOR APPLICATION NUMBER: US/09/821,837
COURSENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 9928
; SOPTWARE: FastSEQ for Wind
; SEQ ID NO 141
; LENGTH: 2645
; TYPE: DNA
; ORGANISM: Herpes simplex
US-08-123-456-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-123-456-141/c
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US-09-821-837-9581
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Matches
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SEQ ID NO 9581
LENGTH: 495
TYPE: DNA
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                            CURRENT APPLICATION NUMBER: US/08/123,456
CURRENT FILING DATE: 1997-03-03
PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR FILING DATE: 1997-06-09
                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(495)
OTHER INFORMATION: n = A,T,C or G
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les 20; Conserv
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                                                                                           FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                          CHAN, JOHN Y.
DABROWSKI-AMARAL,
                                                                                                                                                                                                                                                                                                                  DELVECCHIO, ALFRED MICHAEL DILLON, SUSAN B. LEARY, JEFFREY JOSEPH
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                                                                                                                                                                                                                                                                                                  SUTTON, DAVID
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ilarity 100.0%;
Conservative 0
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Pred. No. 2.8e+02;
0; Mismatches 0;
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Pred. No. 2.8e+02;
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                                                                                   APPLICANT: DILLON, SUSAN B.
APPLICANT: LEARY, JEFFREY JOSEPH
APPLICANT: SUTTON, DAVID
TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
FILE REFERENCE: PS0583
CURRENT APPLICATION NUMBER: US/09/94,404
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/297,477
PRIOR FILING DATE: 1999-6-29
PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR PILING DATE: 1999-11-04
PRIOR PILING DATE: 1999-10-6-09
PRIOR FILING DATE: 1999-10-6-09
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US-09-994-404-141/c
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; ORGANISM: Herpes simplex
US-09-297-477A-141
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                               SOFTWARE: Fa
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SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 141
LENGTH: 2645
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Best Local Similarity
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Best Local
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APPLICANT: CHAN, JOHN Y.
APPLICANT: DABROWSKI-AWARAL,
APPLICANT: DELVECCHIO, ALPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/297,477A CURRENT FILING DATE: 1999-06-29 PRIOR APPLICATION NUMBER: US 60/030,279 PRIOR FILING DATE: 1999-11-04 PRIOR APPLICATION NUMBER: US 60/049,018 PRIOR FILING DATE: 1997-06-09
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APPLICANT: CHAN, JOHN Y.
APPLICANT: DABROWSKI-AMAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL CODING SEQUENCES TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                   LENGTH:
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                                                    FastSEQ for Windows Version 3.0
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DILLON, SUSAN B.
LEARY, JEFFREY JOSEPH
SUTTON, DAVID
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100.0%; Pred. No. 2.9e+02;
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100.0%; Pred. No. 2.9e+02;
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US-08-804-439-13
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                                                                                                                                           RESULT 12
US-09-301-390-13
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                                                                                                        Sequence 13, Applicat GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 29938-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                 APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYC
TITLE OF INVENTION: SUBI
                                                  APPLICANT: Rose, Timothy M. APPLICANT: Bosch, Marnix L. APPLICANT: Strand, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rose, Timothy M. APPLICANT: Bosch, Marnix L.
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 17-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
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Local Similarity 100.0%;
ses 20; Conservative (
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STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                     1988 TCACCACCGTCAGCACCTTC 2007
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                                                                                                                              Application US/09301390
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2713 base pairs
                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB 13; ilarity 100.0%; Pred. No. 2.9e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strand, Kurt
                                                                                                                                                                                                                                                                                                                                                                                              linear
                 GLYCOPROTEIN B OF THE RFHV/KSHV SUBFAMILY OF HERPES VIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13:
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Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                            20
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Length 2713;

Indels

0

Gaps

0,

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Length 2645;
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Indels

0

Gaps

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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,439
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHY/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPDLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/09338326 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/720
PILING DATE: 26-5EP-1996
ATTORNEY/AGENT INFORMATION:

NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 2993
TBLECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
                                                                                                     STATE: CA
COUNTRY: USA
ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/301,390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
              CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/720,229
APPLICATION NUMBER: US 08/720,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: CA
                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Morrison & Foerster STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
26-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB 19; 100.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                        100
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                                                                                             US/09/338,326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 15
US-08-123-456-78
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SEQ ID NO 11
LENGTH: 2715
TYPE: DNA
ORGANISM: HERPES VIRUS, TYPE 1
US-60-412-956-11
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US-60-412-956-11
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Matches
                                                                                                                                                                                                           Sequence 78, Application US/08123456
GENERAL INFORMATION:
APPLICANT: ESSER, KLAUS M.
APPLICANT: CHAN, JOHN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/60412956 GENERAL INFORMATION:
                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SYEES, KATHRYN F.

APPLICANT: STEMKE-HALE, KATHERINE
APPLICANT: JOHNSTON, STEPHEN ALBERT
TITLE OF INVENTION: MUTCHEN AND COMPOSITIONS FOR VACCINATION COMPRISING
TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF THE
TITLE OF INVENTION: HERPESVIRUS FAMILY
FILE REFERENCE: MCRO:002USP1
CURRENT APPLICATION NUMBER: US/60/412,956
CURRENT FILING DATE: 2002-09-23
NUMBER OF SEQ. ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
FILE REFERENCE: P50583
CURRENT APPLICATION NUMBER: US/08/123,456
CURRENT FILING DATE: 1997-03-03
PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR FILING DATE: 1999-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                           APPLICANT:
                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (%1.706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        Match 100.0%; S
Local Similarity 100.0%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                     ESSER, KLAUS M.
CHAN, JOHN Y.
DABROWSKI-AMARAL,
                                                                                                                                                                                                                                                                                                                                                         TCACCACCGTCAGCACCTTC 2010
                                                                                                                        DILLON, SUSAN B.
LEARY, JEFFREY JOSEPH
SUTTON, DAVID
                                                                                                                                                                           DABROWSKI-AMARAL, CHRISTINE ELLEN DELVECCHIO, ALFRED MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 19; ilarity 100.0%; Pred. No. 2.9e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                      NOVEL CODING SEQUENCES FROM HERPES SIMPLEX VIRUS TYPE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40,253
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 96;
Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2715;
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Minimum
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Maximum Match 100%
Listing first 45 g
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Perfect score:
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    is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USO7_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*
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84.0 2527
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84.0 2731748
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82.0 207149
82.0 207149
82.0 273174
79.0 173
79.0 743
79.0 772
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Gapop 10.0 , Gapext 1.0
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                                       US-60-487-610-1969
US-60-495-114-16937
US-60-487-610-19377
US-10-425-114A-19377
US-10-425-114A-19377
US-10-425-114A-26570
US-10-425-114A-26570
US-10-425-114A-26570
US-10-425-114A-26570
US-10-425-114A-26570
US-10-425-114A-26570
US-10-425-114A-26570
US-10-425-114A-29130
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US-60-490-890-2916
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US-09-654-936A-147

US-60-487-610-19444

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chance to have a result being printed,
                                                            Sequence 147, App Sequence 1944, A Sequence 19409, A Sequence 19609, A Sequence 19377, A Sequence 19377, A Sequence 115, App Sequence 115, App Sequence 26075, A Sequence 2530, A Sequence 24003, A Sequence 24003, A Sequence 24003, A Sequence 24000, A Sequence 24312, App Sequence 24312, App Sequence 24316, App Sequence 2216, App Sequence 2216, App Sequence 19647, Ap
Sequence 75,
Sequence 1082:
Sequence 1177:
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Sequence
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| | Ω. | (1 | | | a | | | | | | | Ω | | | | G | | |
| 5 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 3 | 30 | 29 | 28 | |
| 15 | 15 | 15 | 15 | 15 | 15.2 | 15 | 15 | 15 | 15.2 | 15.2 | 15 | 15 | 15.4 | 15 | 15 | 15.4 | 15 | |
| N | 'n | 'n | 'n | 'n | | 'n | 'n | 'n | N | 'n | 4 | ٠. | ٠. | ٠. | A. | • | <u>.</u> | |
| 76. | 76. | 76.0 | 76. | 76.0 | 76.0 | 76.0 | 76.0 | 76. | 76. | 76. | 77. | 77.0 | 77. | 77. | 77. | 77.0 | 77. | |
| 0 | ٥ | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | | | | | | | |
| 20: | 20: | 20: | 201 | 20: | 20: | 201 | 201 | 201 | 20: | 20: | 273174 | 513030 | 255673 | 255673 | 201007 | 76798 | 202 | |
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| US-60-487-610-7028: | US-60-487-610-69753 | US-60-487-610-69747 | US-60-487-610-69730 | US-60-487-610-69700 | US-60-487-610-69696 | US-60-487-610-58562 | US-60-487-610-40116 | US-60-487-610-40115 | US-60-487-610-40114 | US-60-487-610-40113 | US-10-297-465B-1 | US-60-487-610-19737 | US-60-495-135-3613 | US-60-495-114-16366 | US-60-487-610-1943 | US-60-490-890-1467 | US-10-425-114A-1061 | |
| 0-4 | 0-4 | 0-4 | 0-4 | 0-4 | 0-4 | 0-4 | 0-4 | 0-4 | 0-4 | 0-4 | 10- | 0-4 | 0-4 | 9-4 | 0-4 | 0-4 | 0-4 | |
| 87- | 87- | 87- | 87- | 87- | 87- | 87- | 87- | 87- | 87- | 87- | 297 | 87- | 95 | 95- | 87- | 90- | 25- | |
| 610 | 610 | 610 | 610 | 610 | 019 | 610 | 610 | 610 | 610 | 610 | -46 | 610 | 135 | 114 | 610 | 990 | 114 | |
| -70 | -69 | -69 | -69 | -69 | -69 | -58 | -40 | -40 | -40 | -40 | 5B- | -19 | -36 | -16 | -19 | -14 | A-1 | |
| 283 | 753 | 747 | 730 | 700 | 696 | 562 | 116 | 115 | 114 | 113 | ۳ | 737 | 13 | 366 | 435 | 67 | 061 | |
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| 70283, | 69753, | 69747, | 69730, | 69700, | 69696, | 58562, | 40116, | 40115, | 40114, | 40113, | 1, Appl: | 737, | 3613, | 16366, | 19435, | 1467, | 611, | |
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ALIGNMENTS

Application US/10425114A

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

FITTLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILLE REPERENCE: 38-21(5313)B

CURRENT TILING DATE: US/10/425,114A

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 27295

LENGTH: 527

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

FEA
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21287, Appl. GENERAL INFORMATION:
              APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Vangwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
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    NUMBER OF
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18; Conserv
SEQ ID NOS: 73128
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Pred. No. 1.1e+02;
D; Mismatches 2;
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0 0 0 0 0 0 0

SEQ ID NO 21287 LENGTH: 2086

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APPLICANT: Drmanac, Radoje T.

ITILE OF INVENTION: Novel Nucleic Acids and
ITILE OF INVENTION: Polypeptides
FILE REFERENCE: 787CIP2C
CURRENT APPLICATION NUMBER: US/09/654,936A
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/466,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR PILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 164
SOPTWARE: pt_FL_genes Version 1.0
SEQ ID NO 147
LENGTH: 7838
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; OTHER INFORMATION: Clone ID: LIB3279-218-A5_FLI
US-10-425-114A-21287
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; LOCATION: (673)..(2616)
US-09-654-936A-147
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                                                                                                                                                                      US-60-487-610-19444
       Sequence 19444, Application US/60487610

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEBATITIS C VIRUS-1
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
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Best Local S
Matches 18
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Best Local Similarity
Matches 18; Conserv
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CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo mapiens
FEATURE:
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                                                                                                                                                                                                                                       TCACCACCATCAGCACCCTC 6480
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Xue, Aldong J.
Wehrman, Tom
Wang, Jian-Rui
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Ren, Feiyan
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Zhou, Ping
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2003-07-17
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Pred. No. 1.1e
0; Mismatches
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Pred. No. 1.1e+02;
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                                                                 VIRUS-INFECTED SUBJECTS
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APPLICANT: Simpson, Andrew
APPLICANT: Reinach, Fernando
APPLICANT: Retubal, Joao
APPLICANT: Medianis, Joao
APPLICANT: Arruda, Paulo
FILE REPERENCE: FAPESP 202 US (10213376)
CURRENT APPLICATION NUMBER: US/10/297,465B
CURRENT APPLICATION NUMBER: US/10/297,465B
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: PCT/IB01/01618
PRIOR FILING DATE: 2001-06-07
PRIOR PILLING DATE: 2001-06-17
PRIOR PILLING DATE: 2001-06-17
NUMBER OF SEQ ID NOS: 1
NUMBER OF SEQ ID NOS: 1
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NAME/KEY: misc feature

; LOCATION: (1)...(91672)

; OTHER INFORMATION: n = A,T,C or G,

US-60-487-610-19444
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US-60-487-610-19609
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                                                                                                                                                                                           Sequence 19609, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
LENGTH: 2731748
TYPE: DNA
ORGANISM: Xylella fastidiosa
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SOFTWARE: FRBEISEQ for Windows Version
SEQ ID NO 19444
LENGTH: 91672
                                       FILE REFERENCE: CLO01469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 19609
LENGTH: 25086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10297465B GENERAL INFORMATION:
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Best Local
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Best Local Similarity
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ORGANISM: Homo sapiens
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90.0%;
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Pred. No. 1
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86537 TCACCACCATCAGCACCT 86520

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US-60-487-610-19377/c
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US-60-495-114-16832
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CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16832, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC
TITLE OF INVENTION: ENCODING HUMAN PROTEASE
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 19377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19377, Appl. GENERAL INFORMATION:
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Best Local
                                                                          Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                     APPLICANT: CARGILL, Michele
APPLICANT: HUANG, HONG'IN
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-1
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILD REPERENCE: CLO01469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KBY: misc_feature
LOCATION: (1)...(25474)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1.
                                                                                                                                           PEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(207149)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1.
                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                        ENGTH: 207149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 CACCACCATCAGCACCTT 315
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17; Conserv
                                                         l Similarity
17; Conserv
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Similarity 94.4%;
   TCACCACCGTCAGCACCT
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                                                                          82.0%;
94.4%;
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94.4%;
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Pred. No. 1.7e+02;
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Pred. No. 1.7e+02;
                                                                        Score 16.4; DB 7; Length 207149; Pred. No. 1.7e+02;
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PROTEINS, METHODS OF DETECTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 25474;
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PCT-US02-37235-115
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Sequence 115, Application PC/TUS0237235
GENERAL INFORMATION:
APPLICANT: Handfield, Martin
APPLICANT: Hillman, Jeffrey
APPLICANT: Progulske-Fox, Ann
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APPLICANT: Regulome Corporation
TITLE OF INVENTION: Functional Sites
FILE REFERENCE: 11207-029-228
FURRENT APPLICATION NUMBER: PCT/US03/18714
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/387,887
PRIOR FILING DATE: 2002-06-13
PRIOR PPLICATION NUMBER: US 60/387,910
PRIOR APPLICATION NUMBER: US 60/387,910
PRIOR PPLICATION NUMBER: US 60/387,910
PRIOR APPLICATION NUMBER: US 60/387,910
PRIOR PILING DATE: 2002-06-13
NUMBER OF SEO ID NOS: 51999
SOPTWARE: PatentIn version 3.2
SEQ ID NO 26075
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US-10-425-114A-19377/c
IS-10-425-114A-19377, Application US/10425114A
GENERAL INFORMATION:
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; LENGTH: 614
; TYPE: DNA
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Matches 17; Conserva
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
FULL REFERENCE: 38-21(53313)B
FULL REFERENCE: 2003-2010
FULL REFERENCE: 2003-20
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mes 16; Conserv
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29
                                                           2 CACCACCGTCAGCACCTTC
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Kovalic, David I
Screen, Steven I
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Pred. No. 3e+02;
                                                                                                                                      Mismatches
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US-10-425-114A-7593/c
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7593
LENGTH: 749
LENGTH: 749
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CURRENT APPLICATION NUMBER: PCT/US02/37235
CURRENT FILING DATE: 2003-06-16
NUMBER OF SEQ ID NOS: 234
SOPTWARE: Patentin version 3.0
SEQ ID NO 115
                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT. VA.
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Best Local :
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GENERAL INFORMATION
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Best Local Similarity
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)18
FILE REFERENCE: 38-21(5313)18
CURRENT APPLICATION NUMBER: US/10/425,114A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Actinobacillus actinomycetemcomitans
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LOCATION: (1)
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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89.5%;
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89.5%;
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Pred. No. 3e
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; OTHER INFORMATION: Clone ID: LIB3029-011-F8_
US-10-425-114A-14861
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SEQ ID NO 26570
LENGTH: 784
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SEQ ID NO 14861
LENGTH: 772
TYPE: DNA
ORGANISM: Glycine max
                                                                                    NUMBER OF SEQ ID NOS:
SEQ ID NO 24003
LENGTH: 919
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                   Sequence 24003, Application US/10425114A GENERAL INFORMATION:
                                                                                                                                         APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihuai
APPLICANT: Zhou, Yihuai
APPLICANT: Kovahic, David K.
APPLICANT: Kovahic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
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                                               TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: LIB4315-040-D4_FLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                FEATURE:
          OTHER INFORMATION: Clone ID: LIB3606-055-G3_FLI
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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Pred. No. 3e
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Pred. No. 3e
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Minimum
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Maximum Match 100%
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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                     33363688 seqs, 16581889874 residues
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18
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Copyright (c) 1993 - 2003
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444 / /cgm2 6/ptcodata/2/pna/US101A, COMB. seq; 45: /cgm2 6/ptcodata/2/pna/US101A COMB. seq; 46: /cgm2 6/ptcodata/2/pna/US101A COMB. seq; 47: /cgm2 6/ptcodata/2/pna/US101A COMB. seq; 48: /cgm2 6/ptcodata/2/pna/US101A COMB. seq; 59: /cgm2 6/ptcodata/2/pna/US10A COMB. seq; 59
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | esult Score | | Query Query Match Length DB ID | 25 B | SUMMARIES DB ID 25 US-09-594-065-2 | Description Sequence 2, Appli |
|---------------|-------------|-------|--------------------------------|--------|--------------------------------------|----------------------------------|
| , <u>,</u> | 18 | 100.0 | 18 | 25 | US-09-594-065-2 | Sequence 2, Appli |
| N | 18 | 100.0 | | 25 | US-09-594-065-9 | Sequence 9, Appli |
| c u | 18 | 100.0 | | 25 | US-09-594-065-12 | Sequence 12, Appl |
| n 4 | 18 | 100.0 | | 25 | 25 US-09-594-065-13 | Sequence 13, Appl |

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Sequence 2, Application US/09594065
; GENERAL INFORMATION:
APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBols, Dwight
TITLE OF INVENTION: Compositions, methods and Kits for Herpes Simplex Virus Type
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE; 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence
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US-09-594-065-2
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                                                                       ; OTHER INFORMATION: Reverse PCR primer US-09-594-065-2
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Matches 18
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13 US-09-777-317-8

17 US-09-892-227-8

18 US-60-082-302-601

19 PCT-US-02-25943-35472

18 US-10-367-832A-35472

10 US-60-452-680-71403
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13 US-09-394-404-141
13 US-08-804-439-13
19 US-09-313-326-13
19 US-09-313-326-13
19 US-09-313-456-78
10 US-09-297-477A-78
10 US-09-297-477A-217
10 US-09-297-477A-217
10 US-09-297-477A-217
10 US-09-297-47A-217
10 US-09-297-688-8
10 US-09-297-688-8
10 US-09-297-288-1201
10 US-10-366-683-1243
10 US-10-366-683-1243
10 US-10-366-683-1362
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US-09-821-837-9581
US-08-123-456-141
                                         Score 18;
Pred. No.
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                               Mismatches
                                      3e+02;
                                                 DB 25; Length 18
                               Indels
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Sequence 1201, Ap
Sequence 7812, Ap
Sequence 7812, Ap
Sequence 7812, Ap
Sequence 7812, Ap
Sequence 1243, Ap
Sequence 1243, Ap
Sequence 1362, Ap
Sequence 1362, Ap
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 601, App
Sequence 601, App
Sequence 35472, A
Sequence 35472, A
Sequence 35472, A
Sequence 71403, A
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Sequence 9581, App
Sequence 141, App
Sequence 141, App
Sequence 141, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 77, Appl
Sequence 77, Appl
Sequence 217, Appl
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; Sequence 12, Application US/09594065
; GENERAL INFORMATION:
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US-09-594-065-9
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US-09-594-065-13/c
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Best Local S
Matches 18
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Best Local S
Matches 18
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Local Similarity 100.0%;
hes 18; Conservative (
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APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and Kits for
TITLE OF INVENTION: Mucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 73
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WhlkerPeach, Cindy:
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and Kit
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence amplified by PCR
US-09-594-065-12
Sequence 13, Application US/09594065
GENERAL INFORMATION:
APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
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Pred. No. 3.1
0; Mismatches
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Pred. No.
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ches 0;
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APPLICANT: HOILZMAN, DOUGLAS A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2076-001
CURRENT APPLICATION NUMBER: US/09/821,837
CURRENT APPLICATION NUMBER: US/09/821,837
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/193,481
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 9928
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9580
LENGTH: 481
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-594-065-14/c
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; OTHER INFORMATION: Sequence amplified by PCR for HSV type-2
US-09-594-065-13
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NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 13
LENGTH: 109
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-09-821-837-9580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WalkerPeach, Cindy
APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and Kits for Herpes Simplex Virus Type 1 an
TITLE OF INVENTION: Nucleic Acid Detection
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 109
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                               Sequence 9580, Application US/09821837 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09594065 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gearing, David P. APPLICANT: Holtzman, Dougla
NAME/KEY: misc feature
LOCATION: (1)...(481)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Sequence amplified by PCR for IAC
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NOS: 14
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100.0%; Pred. No. 3.1e+02;
htive 0; Mismatches 0;
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US-09-821-837-9581/c
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                                                                                              SOFTWARE: F
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                LENGTH: 2645
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APPLICANT: HOLLTON, Douglas A.
APPLICANT: HOLLTON, DOUGLS ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR F.
FILE REFERENCE: 1600.2076-001
CURRENT APPLICATION NUMBER: US/09/821,837
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/193,481
PRIOR APPLICATION NUMBER: US 60/193,481
PRIOR FILING DATE: 2000-03-9
INUMBER OF SEQ ID NOS: 9928
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9561
LENGTH: 499
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:

, NAME/KEY: misc feature

; LOCATION: (1). (495)

; OTHER INFORMATION: n = A,T,C

US-09-821-837-9581
; TYPE: DNA
; ORGANISM: Herpes simplex
US-08-123-456-141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9581, Application US/09821837 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR TILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gearing, David P. APPLICANT: Holtzman, Dougla
                                                                                                                                                                                                                         CURRENT FILING DATE: 1997-03-03
                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: P50:
                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 AGCAGGCCGCTGTCCTTG 250
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                                                                                                    FastSEQ for Windows, Version 3.0
                                                                                                                                                                                                                                                                                                                                DELVECCHIO, ALFRED MICHAEL
DILLON, SUSAN B.
LEARY, JEFFREY JOSEPH
SUTTON, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                   DABROWSKI-AMARAL,
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                                                                                                                                                                                                                                                                       P50583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLAUS M.
                                                                                                                                                                                                                                                                                         NOVEL CODING SEQUENCES FROM HERPES SIMPLEX VIRUS TYPE-2
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CURRENT APPLICATION NUMBER: US/09/297,477A
CURRENT FILING DATE: 1999-06-29
FRIOR APPLICATION NUMBER: US 60/030,279
FRIOR APPLICATION NUMBER: US 60/049,018
FRIOR APPLICATION NUMBER: US 60/049,018
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 303
SOPTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 141
LENGTH: 2645
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Best Local S
Matches 18
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                                  SEQ ID NO 141
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Best Local Similarity
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APPLICANT: DILLON, SUSAN B.
APPLICANT: LEARY, JEFFREY JOSEPH
APPLICANT: SUTTON, DAVID
TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
FILE REFERENCE: P50583
                                                                                            PRIOR APPLICATION NUMBER: 09/297,477
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                                                        FILE REFERENCE: P50583
CURRENT APPLICATION NUMBER: US/09/994,404
CURRENT FILING DATE: 2001-11-26
                                                                                                                                                                                                                                                                             APPLICANT: DILLON, SUSAN B.
APPLICANT: LEARY, JEFPREY JOSEPH
APPLICANT: SUTTON, DAVID
TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DABROWSKI-AMARAL, APPLICANT: DELVECCHIO, ALFRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ESSER, KLAUS M. APPLICANT: CHAN, JOHN Y.
                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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TYPE: DNA
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                                                       FastSEQ for Windows Version 3.0
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100.0%; Pred. No. 3.5e+02;
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100.0%; Pred. No. 3
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ALFRED MICHAEL
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                                                                                                                                    RESULT 12
US-09-301-390-13/c
                                                                                                                                                                                                                                                                                                                                                  US-08-804-439-13
                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 18
                                             Sequence 13, Application US/09301390
GENERAL INFORMATION:
APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,439
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 29:
TELECOMMUNICATION INFORMATION:
TELECOMONE //**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff J. Michael
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rose,
APPLICANT: Bosch
APPLICANT: Stran
                  TITLE OF INVENTION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304-1018
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Local Similarity 100.0%; F
les 18; Conservative 'Q;
                                                                                                                                                                                                                                                                              Local Similarity 100. es 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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STREET: 755 Page Mill Road
                                                                                                                                                                                                           2096 AGCAGGCCGCTGTCCTTG 2079
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Bosch, Marnix L.
Strand, Kurt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 813-5600
                GLYCOPROTEIN B OF THE RFHV/KSHV SUBFAMILY OF HERPES VIRUSES
                                                                                                                                                                                                                                                                              100.0%; Score 18; DB 13;
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
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Pred. No. 3.5e+02;
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

5: Morrison & Foerster

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09338326 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                        CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/720
PILING DATE: 26-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J Michael
REGISTRATION NUMBER: 40,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: (415) 494-0/94
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/720,229
APPLICATION 26-SEP-1996
                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: SUBPAMILY OF HERPES VIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 29938-20002.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/301,390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: FIR PC-DOS/MS-DOS
COPTRAING SYSTEM: PC-DOS/MS-DOS
COPTRAINE: Pat-17-PC-1006/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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APPLICANT: SULLEY NOVEL CODING STATES OF INVENTION: SIMPLEX VIRUS TYPE-2; TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2; FILE REFERENCE: P50583
CURRENT APPLICATION NUMBER: US/08/123,456; CURRENT FILING DATE: 1997-03-03; PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR APPLICATION NUMBER: US 60/030,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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US-08-123-456-78/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: HERPES VIRUS, TYPE 1
US-60-412-956-11
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Matches
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LENGTH: 2715
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                 Sequence 78, Application US/08123456 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SYKES, KATHRYN F.
APPLICANT: STEMKE-HALE, KATHERINE
APPLICANT: JOHNSTON, STEEDHEN ALBERT
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPBPTIDE SEQUENCES OF THE
TITLE OF INVENTION: HERRESVIRUS FAMILY
FILE REFERENCE: MCRO:002USP1
CURRENT APPLICATION UNMEER: US/60/412,956
CURRENT FILING DATE: 2002-09-23
RUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 299
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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100.0%; Score 18; DB 96;
Local Similarity 100.0%; Pred. No. 3.5e+02;
es 18; Conservative 0; Mismatches 0;
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                                                                                                                                               DILLON, SUSAN B.
LEARY, JEFFREY JOSEPH
SUTTON, DAVID
                                                                                                                                                                                                     DABROWSKI-AMARAL, CHRISTINE ELLEN DELVECCHIO, ALFRED MICHAEL
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                              KLAUS M.
                                                                                                            NOVEL CODING SEQUENCES FROM HERPES SIMPLEX VIRUS TYPE-2
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Pred. No. 3.5e+02;
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Sequence 35800, A
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Sequence 1679, Ap
Sequence 281804, A
Sequence 281804, A
Sequence 31551, A
Sequence 5, Appli
Sequence 16659, A
Sequence 16659, A
Sequence 16651, A
Sequence 16541, A
Sequence 16451, A
Sequence 19295, A
Sequence 1946, A
Sequence 1946, A
Sequence 1941, A
Sequence 1943, A
Sequence 1943, A
Sequence 18631, A
Sequence 16451, A
Sequence 113, App

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
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length: 2000000000
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Query
Match Length
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18
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| cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
| cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
| cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
| cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
| cgn2_6/ptodata/2/pna/US00_NEW_COMB.seq:*
| cgn2_6/ptodata/2/pna/US00_NEW_COMB.seq:*
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   agcaggccgctgtccttg
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US-10-651-237-4
US-60-495-114-38730
US-60-495-114-89612
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US-10-425-114A-26939
US-10-425-114A-26285
US-10-425-114A-16387
US-60-495-114-16387
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16387 A
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Sequence 4, Application US/10651237

GENERAL INFORMATION:

APPLICANT: Ortho-Clinical Diagnostics, Inc.

APPLICANT: Wang, Yixin

ITILE OF INVENTION: Colorectal Cancer Prognostics

FILE REFERENCE: ADS-5003 US NP

CURRENT APPLICATION NUMBER: US/10/651,237

CURRENT FILING DATE: 2003-08-27

NUMBER OF SEQ ID NOS: 94

SOFTWARE: PatentIn version 3.1

SOFTWARE: PatentIn version 3.1

LENGTH: 1924

TYPE: DNA
ORGANISM: human
                                                                                                                                                                        RESULT 2
US-10-651-237-7/c
Sequence 7, Application US/10651237
Sequence 7, Application US/10651237
GENERAL INFORMATION:
APPLICANT: Ortho-Clinical Diagnostics, Inc.
APPLICANT: Wang, Yixin
TITLE OF INVENTION: Colorectal Cancer Prognostics
FILE REFERENCE: ADS-5003 US NP
CURRENT APPLICATION NUMBER: US/10/651,237
CURRENT FILING DATE: 2003-08-27
NUMBER OF SEQ ID NOS: 94
                                                                      SOFTWARE: PatentIn version 3.1'; SEQ ID NO 7; LENGTH: 1924; TYPE: DNA ; ORGANISM: human
US-10-651-237-7
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Matches 17; Conserv
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Matches 17; Conserv
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US-10-425-114A-33240
US-60-495-114-1078
US-10-425-114A-21804
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US-10-425-114A-218151
US-60-485-114A-26843
US-10-425-114A-26843
US-60-487-610-19295
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US-60-487-610-19846
US-60-487-610-19846
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US-60-487-610-19846
US-60-487-610-19846
US-60-487-610-19846
US-60-487-610-186638
US-10-084-846A-107
               Score 16.4; DI
Pred. No. 65;
0; Mismatches
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Pred. No. 65;
0; Mismatches
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Scoring table:

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RESULT 5
US-60-495-114-89619/c
US-60-495-114-89619/c
; Sequence 89619, Application US/60495114
; GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC AC:
TITLE OF INVENTION: ENCODING HIMAN PROTEASE PROFILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
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; ORGANISM: Homo sapiens
US-60-495-114-38730
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; ORGANISM: Homo sapiens
US-60-495-114-89612
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Best Local S
Matches 16
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Sequence 38730, Application US/60495114

APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480

CURRENT APPLICATION NUMBER: US/60/495,114

CURRENT FILING DATE: 2003-08-15

NUMBER OF SEQ ID NOS: 91238

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 38730

LENGTH: 201
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CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 89612
LENGTH: 201
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
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94.1%;
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94.1%;
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Pred. No. 2.2e+02;
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Pred. No. 2.
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PROTEINS, METHODS OF DETECTION AND
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; ORGANISM: Homo sapiens
US-60-495-114-89619
                                                                                                                                                                                                                 APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yonguri
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; OTHER INFORMATION: Clone ID: LIB4676-059-G1_FLI US-10-425-114A-26959
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Best Local Similarity
Matches 16; Conserv
                                                                                 NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26959
LENGTH: 2463
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LENGTH: 201.
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Best Local Similarity
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                                                                                                                                   APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
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                                              ORGANISM: Homo sapiens
                                                                    TYPE: DNA
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                                  FEATURE:
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Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
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94.1%;;
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Pred. No. 2.2e
0; Mismatches
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Pred. No. 1.
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APPLICANT: Li, Martha
APPLICANT: Rupnow, Brent A.
APPLICANT: Webster, Kevin R.
APPLICANT: Jackson, Donald
APPLICANT: Wong, Tai W.
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-490-890-1861
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                                                                                                                                 US-10-425-114A-26285
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                                                                                                                                                                                                                 SEQ ID NO 26285
LENGTH: 2487
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Best Local :
                                                                Matches
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                                                                                                Query Match
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                                                                                                                                                                                                                                           APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT FILING DATE: 2003-04-28
TUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION FILE REFERENCE: D0310 PSP CURRENT ADJUCATION NUMBER: US/60/490,890 CURRENT FILING DATE: 2003-07-29 NUMBER OF SEQ ID NOS: 2779 NUMBER OF SEQ ID NOS: 2779 SOPTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liu, Jingdong
                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                               OTHER INFORMATION: Clone ID: LIB4119-174-G9_FLI
                                                                                                                                                                  FEATURE:
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                                                                                Similarity
                             AGCAGGCCGCTGTCCTT 17
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                                                                Conservative
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Pred. No. 1.9e+02;
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                                                                              Score 15.4; DB 6;
Pred. No. 1.9e+02;
                                                              Mismatches
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                                                                                              DB 6;
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                                                                                          Length 2487;
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RESULT 10

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(26433)
; OTHER INFORMATION: n = A,T,C or G,
US-60-495-114-16387
                                                                                                                                RESULT 12
US-60-495-114-16957/c
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US-60-495-114-16387/c
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 09/473,646
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: US 60/050,356
PRIOR FILING DATE: 1997-06-20
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TITLE OF INVENTION: POLYMO
TITLE OF INVENTION: ENCOD
TITLE OF INVENTION: USES
FILE REFERENCE: CL001480
            Sequence 16957, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NI
TITLE OF INVENTION: ENCODING HUMAN PROTITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16387
LENGTH: 26433
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APPLICANT: Cooper, Mark J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16387, Application US/60495114 GENERAL INFORMATION:
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Best Local
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FILE REFERENCE: CL001480
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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ORGANISM: Homo
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                Michele
POLYMORPHISMS IN NUCLEIC
ENCODING HUMAN PROTEASE
USES THEREOF
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94.1%;
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94.1%;
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Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                      Score 15.4; DB 7; Length 26433; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                or insertion/deletion polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACID MOLECULES
PROTEINS, METHODS OF DETECTION AND
                                                    ACID MOLECULES
                                  PROTEINS, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2799;
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                                    OF DETECTION
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RESULT 13
US-60-495-114-16382/c
US-60-495-114-16382/c
US-60-495-114-16382/c
ISEQUENCE 16382, Application US/60495114

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
ITITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
ITITLE OF INVENTION: USES THEREOF
ITITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01480
CURRENT APPLICATION UMMBER: US/60/495,114
CURRENT PILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 16382
LENGTH: 384485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-60-495-114-16382
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Green, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 27906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16957
                                                                                                                                                                                                                                                                             Sequence 27906, Application US/10425114A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(384485)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(45664)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 45664
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                                                                                                                                                                                                                                                                                                                                                                                                          376152 AACAGGCCGCTGTCCTT 376136
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGCAGGCCGCTGTCCTT 17
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Similarity 94.1%;
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94.1%;
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Pred. No. 1.6e+02;
0; Mismatches 1
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LENGTH: 1529

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TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC TITLE OF INVENTION: ENCODING HUMAN PROTEASE; TITLE OF INVENTION: USES THEREOP FILE REFERENCE; CL001480

CURRENT APPLICATION NUMBER: US/60/495,114

CURRENT FILING DATE: 2003-08-15

NUMBER OF SEQ ID NOS: 91238

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4742-003-G8_FLI
US-10-425-114A-27906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-60-495-114-15241/c
; Sequence 15241, Application US/60495114
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Search completed: September 16, 2003, Job time : 30.3366 secs
                                                                      밁
                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-60-495-114-15241
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                      Query Match 82.2%;
Best Local Similarity 88.9%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CARGILL,
                                                                                                                                                                                                                                           LENGTH: 201
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 GCÁGGCCGCTGTCCT 141
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                                                                      65 AGCAGGCCGGTGTGCTTG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GCAGGCCGCTGTCCT 16
                                                                                                     1 AGCAGGCCGCTGTCCTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                   POLYMORPHISMS IN NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, METH
                                                                                                                                                                                                                                                                                                                                                                                                                                        Michele
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100.0%; Pred. No. 3.1e+02
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                                                                                                                                                        Score 14.8; DB 7
Pred. No. 4.3e+02
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                   22:47:53
                                                                                                                                                                            DB 7;
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                                                                                                                                                                        Length 201;
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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Perfect score:
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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30
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457.275 Million cell updates/sec
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/cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US06_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
/cgn2_6/ptodata/2/pna/US099B_C
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Copyright (c) 1993 - 2003 Compugen
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/2/pna/PCTUS_COMB.seq.old:*
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44. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
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53. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
54. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
55. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
56. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
59. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
60. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
61. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
62. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
63. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
64. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
65. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
66. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
67. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
68. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
69. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
70. /cgn2_6/ptodata/2/pna/USI10Na_COMB.seq:
71. /cgn2_6/ptodata/2/pna/USI011_COMB.seq:
72. /cgn2_6/ptodata/2/pna/USI011_COMB.seq:
73. /cgn2_6/ptodata/2/pna/USI011_COMB.seq:
74. /cgn2_6/ptodata/2/pna/USI011_COMB.seq:
75. /cgn2_6/ptodata/2/pna/USI011_COMB.seq:
76. /cgn2_6/ptodata/2/pna/USI011_COMB.seq:
77. /cgn2_6/ptodata/2/pna/USI012_COMB.seq:
78. /cgn2_6/ptodata/2/pna/USI012_COMB.seq:
79. /cgn2_6/ptodata/2/pna/USI012_COMB.seq:
79. /cgn2_6/ptodata/2/pna/USI013_COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| () | () | | | Result |
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| 20 | 20 | 23 | | Score |
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| 68 | 20.4 68.0 | 79.3 | 100. | Query |
| 0 | ò | ù | 0 | 34 |
| 714 | 714 | 2142 | 30 | Query Match Length DB ID |
| 16 | 51 | 25 | 25 | ₽B |
| US-60-360-039-41285 | US-10-369-493-41285 | US-09-584-852-6658 | US-09-594-065-3 | |
| Sequence 41285, A | Sequence 41285, A | Sequence 6658, Ap | Sequence 3, Appli | * Description |

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                                                                                                  ; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: IAC specific molecular beacon
US-09-594-065-3
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US-09-594-065-3
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                                           Query Match
Best Local S
Matches 30
                                                                                                                                                                                                                             Sequence 3, Application US/09594065
GENERAL INFORMATION:
APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and Kits for Herpes Simplex Virus Type 1
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT FILING DATE: 2000-06-14
                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 30
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                                           Similarity
30; Conserv
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18 US-09-270-843B-77960
18 US-09-270-849B-51162
51 US-10-366-683-6704
52 US-10-419-128-6539
51 US-10-419-128-6599
52 US-10-149-128-6599
52 US-10-148-712-8606
53 US-10-144-711-8606
91 US-60-360-207-8606
91 US-10-144-771-8606
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52 US-10-419-128-6539
53 US-10-419-128-6539
147 US-10-156-523-96
18 US-09-270-849B-65208
19 US-09-521-640-194436
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19 US-09-521-640-19436-5097
19 US-09-605-703B-1951
19 US-09-191-989-1
10 US-09-191-989-1
10 US-09-191-989-2
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10 US-09-528-237A-1860
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                                                                      Length 30;
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Sequence 77960, A
Sequence 77960, A
Sequence 5704, Ap
Sequence 6704, Ap
Sequence 6704, Ap
Sequence 6599, Ap
Sequence 6599, Ap
Sequence 6599, Ap
Sequence 6204, Ap
Sequence 6204, Ap
Sequence 6204, Ap
Sequence 6619, Appl
Sequence 6639, Ap
Sequence 6639, Ap
Sequence 6639, Ap
Sequence 6678, Appl
Sequence 6578, Ap
Sequence 6578, Ap
Sequence 96, Appl
Sequence 91, Appl
Sequence 91, Appl
Sequence 119436, A
Sequence 119436, A
Sequence 119436, A
Sequence 21582, A
Sequence 21582, A
Sequence 21582, A
Sequence 56997, A
Sequence 3, Appli
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                                            Gaps
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 RESULT 4
US-60-360-039-41285/c
J Sequence 41285, Application US/60360039
GENERAL INFORMATION:
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Best Local S
Matches 25
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Matches
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Starfeng
TITLE Coldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
SEQ ID NO 41285
LENGTH: 714
TYPE: DNA
CDCANTSM: XVIella fastidiosa
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APPLICANT: Williamson, Mark
TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1118-001
CURRENT APPLICATION NUMBER: US/09/584,852
CURRENT FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/135,618
PRIOR FILING DATE: 1999-05-24
PRIOR PPLICATION NUMBER: 60/135,711
PRIOR PILING DATE: 1999-05-24
PRIOR FILING DATE: 1999-05-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-369-493-41285/c Sequence 41285, Application US/10369493 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-09-584-852-6658
                                                                                                                                                                                                                                                                                     ; ORGANISM: Xylella fastidiosa
US-10-369-493-41285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 CCTGCGTAGTGGTAGGCCCTCCTGCAG 472
2 CCTGCGTAGTGGTACGACCTCCTGCAG 28
                                                                                                                                            Similarity 80.0
24; Conservative
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92.6%;
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Pred. No. 2
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Pred. No. 8.9;
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GENERAL INFORMATION:
APPLICANT: Simpson, Andrew
APPLICANT: Reinach, Pernando
APPLICANT: Restubal, Joao
APPLICANT: Setubal, Joao
APPLICANT: Medianis, Joao
APPLICANT: Arruda, Paulo
TITLE OF INVENTION: Isolated Genome of Xylella Fastidiosa and Uses Thereof
FILE REFERENCE: FAPESP 202 US (10213376)
CURRENT APPLICATION NUMBER: US/10/297,465A
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: PCT/IB01/01618
APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 77960
                                                                                                                                                    Sequence 77960, Application US/09270849B GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 41285
LENGTH: 714
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ORGANISM: Xylella fastidiosa
-60-360-039-41285
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-06-17
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PRIOR APPLICATION NUMBER: 60/209,906
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2731748
TYPB: DNA
ORGANISM: Xylella fastidiosa
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Pred. No. 2.5e+02;
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Pred. No. 5
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US-10-366-683-6704/c
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US-09-270-849B-51162/c
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Best Local Similarity 79.3
Conservative
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CURRENT FILING DATE: 1999-03-17
RUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51162
LENGTH: 376
TYPE: DNA
                                                                                                                                 NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6774
LENGTH: 483
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                    Sequence 6704, Application US/10366683
GENERAL INFORMATION:
APPLICANT: Rubenfield, Marc J.
APPLICANT: Nolling, Jork
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Best Local Similarity
                                                 Best
                                                               Query Match
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                                                                                                                                                                                                TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: PATHO3-04
CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Deloughery, Craig APPLICANT: Bush, David
                                                                                                              TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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                                                 Similarity
CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
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79.3%;
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                               Score 19:4; DB 51;
Pred. No. 6.7e+02;
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Pred. No. 6.
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Pred. No. 2
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Sequence 6599, Application US/10:
GENERAL INFORMATION:
APPLICANT: Rubenfield, Marc J.
APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
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US-10-419-128-6704/c
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US-10-366-683-6599
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ABBUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 196678
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GENERAL INFORMATION:
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Best Local 8
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Best Local S
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CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                  TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS FILE REFERENCE: PATHO3-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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CURRENT APPLICATION NUMBER: US/10/366,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         PERTURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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ilarity 79.3%;
Conservative
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79.3%;
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Pred. No. 6.7e+02
0; Mismatches
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Pred. No. 6.7e+02
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                                     SEQUENCES RELATING AND THERAPEUTICS
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Sequence 6599, Application US/10419128
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: ABBUGINOSA FOR DIAGNOSTICS
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PRIOR FILING DATE: 1995-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6599
LENGTH: 510
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/10/419,128

CURRENT FILING DATE: 2003-04-21

PRIOR APPLICATION NUMBER: US/09/252,991

PRIOR PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27
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LENGTH: 510
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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APPLICANT:
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APPLICANT: Zamuc
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Local Similarity 79.3%;
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                                                                                                      Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                        Trawick, John
                                                                                                                                                                           Wall, Daniel
                                                                                                                                                                                          Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                          Zamudio, Carlo
Malone, Cheryl
                                                                                                                                                                                                                              Haselbeck, Robert
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lio, Carlos
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79.3%;
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Pred. No. 6.7e+02;
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Pred. No. 6.7e+02
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                                                                         Genes in Microorganisms
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US-10-156-761-4750
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                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (1)..(1323)
US-10-156-761-4750
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                                                                   Query Match
Best Local S
Matches 23
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4750
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Matches
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GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
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                                                                                                                                                                                          TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
                                                                                                                                                                                                                                               LENGTH: 1323
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les 23; Conservative
                                                                                     Local Similarity
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APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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FILING DATE: 2000-05-23
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APPLICATION NUMBER: 60/257,931
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FILING DATE: 2000-11-27
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FILING DATE: 2000-09-06
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                    1 CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
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CCCCGGGAAGCGTACGACGTCCTGCTGG 697
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10156761
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                                                                                    64.7%;
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                                                                 Score 19.4; DB 47; Pred. No. 7.3e+02; 0; Mismatches 6;
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                                                                                                    Length 1323;
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CURRENT APPLICATION NUMBER: US/09/489,039A; CURRENT FILING DATE: 2000-01-27; PRIOR APPLICATION NUMBER: US 60/117,747; PRIOR PILING DATE: 1999-01-29; NUMBER OF SEQ ID NOS: 14342; SEQ ID NO 6204; LENGTH: 1368; TYPE: DNA CORGANISM: Klebsiella pneumoniae
Search completed: September 16, 2003, 22:44:55 Job time: 2185.74 secs
                                                                                              밁
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US-09-489-039A-6204
                                                                                                                                                                                                                                                                                US-09-489-039A-6204
                                                                                                                                              Query Match
Best Local Similarity 79.3
Best Local Similarity 79.3
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6204, Application US/09489039A
GENERAL INFORMATION:
APPLICANT: GENERAL SECTION: NUCLEIC ALL
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
                                                                                           771 CCCGGCGTGGTGGCAGGAGTTCCTGCAGG 799
                                                                                                                                       1 CCCTGCGTAGTGGTACGACCTCCTGCAGG 29
                                                                                                                                                                                                        64.7%; Score 19.4; DB 2
79.3%; Pred. No. 7.4e+02
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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| Cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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(c) 1993 - 2003 Compugen Ltd
               US-10-425-114A-33391
US-10-425-114A-3571
US-10-425-114A-19153
US-10-425-114A-28420
US-10-425-114A-28420
US-10-425-114A-21709
US-10-425-114A-11209
US-10-425-114A-11709
US-60-480-590-5114
US-60-485-450-11874
5 US-60-487-610-31672
US-60-487-610-31672
US-60-487-610-31706
7 US-60-485-450-3775
7 US-60-485-450-26392
US-10-425-114A-13077
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Sequence 1, Appli Sequence 33391, Appl Sequence 3571, Appl Sequence 5952, A Sequence 28420, A Sequence 21709, Appl Sequence 21709, Appl Sequence 5114, Appl Sequence 5114, Appl Sequence 3130, Appl Sequence 3130, Appl Sequence 31674, A Sequence 31674, A Sequence 31675, Appl Sequence 31706, A Sequence 31706, A Sequence 31706, A Sequence 31707, A Sequence 31707, A Sequence 5775, Appl Sequence 13077, A Sequence 13031, A Sequence 13031, A Sequence 13031, A Sequence 13031, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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| 7 1224 6 7 8059021 5 201 7 2017 7 2018 7 2052 7 2052 7 2168 5 2189 7 2196 7 2320 7 2336 7 2473 7 2657 7 2653 7 2653 7 2653 7 2653 7 2653 7 2653 7 2653 7 | ٠. | ۰. | | ۰. | | ٠. | 1.1 | | 4.3 | 4.1 | | 1.1 | Ω (3 | 1.1 | 1.3 | 1.3 | | 0 |
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| 5 US-10-296-115-154 5 US-10-296-125-46 7 US-60-487-610-57668 7 US-60-487-610-793 6 US-10-296-115-464 7 US-60-493-007-2834 7 US-60-493-007-2834 7 US-60-487-610-798 7 US-60-487-610-798 7 US-60-487-610-794 7 US-60-487-610-795 7 US-60-487-610-795 7 US-60-487-610-795 7 US-60-487-610-795 7 US-60-487-610-796 7 US-60-487-610-796 7 US-60-487-610-796 7 US-60-487-610-20041 7 US-60-487-610-20041 | 45317 | 26562 | 9041 | 2715 | 2663 | 2657 | 2473 | 2366 | 2320 | 2196 | 2189 | 2168 | 2052 | 2017 | 1981 | 201 | 8059021 | 1224 |
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| | US-60-487-610-19569 | US-60-487-610-20041 | US-60-478-196-332 | US-60-487-610-796 | US-60-487-610-792 | US-60-487-610-791 | US-60-487-610-795 | US-60-487-610-794 | US-60-487-610-788 | US-60-487-610-790 | US-60-487-610-789 | US-09-908-576-331 | US-60-493-007-2834 | US-10-296-115-464 | US-60-487-610-793 | US-60-487-610-57668 | US-09-947-914-53 | US-10-296-115-154 |
| | 19569, A | 20041, A | • | • | 792, App | 791, App | 795, App | | 788, App | | 789, App | • | 2834, Ap | 464, App | 793, App | Sequence 57668, A | Sequence 53, App. | 154, App |

ALIGNMENTS

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RESULT 2
US-09-947-914-75
; Sequence 75, Application US/09947914
; GENERAL INFORMATION:
GENERAL INFORMATION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON FILE REFERENCE: CL001298
; CURRENT APPLICATION NUMBER: US/09/947,914
; CURRENT FILING DATE: 2001-09-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465B-1
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US-10-297-465B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10297465B GENERAL INFORMATION:
                                                                 NUMBER OF SEQ ID NOS: 75
SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.2 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Simpson, Andrew
APPLICANT: Reinach, Fernando
APPLICANT: Reinach, Fernando
APPLICANT: Setubal, Joao
APPLICANT: Setubal, Joao
APPLICANT: Medianis, Joao
APPLICANT: Medianis, Joao
APPLICANT: Mruda, Paulo
TITLE OP INVENTION: Isolated Genome of Xylella Fastidiosa and Uses Thereof
FILE REFERENCE: FAPESP 202 US (10213376)
CURRENT APPLICATION NUMBER: US/10/297,465B
CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 607/1801/01618
PRIOR APPLICATION NUMBER: 60/209,906
PRIOR APPLICATION NUMBER: 60/209,906
PRIOR FILING DATE: 2001-06-17
NUMBER OF SEQ ID NOS: 1
ORGANISM: HUMAN
                        LENGTH: 4813087
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                 1446654 CCCTGCGCATCGGTTCGACCTTGTGCAGGG 1446683
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mes 24; Conserva
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ilarity 80.0%;
Conservative
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; NAME/KEY: misc_feature; LCATION: (1)...(4813087); COTHER INFORMATION: n = A,T,C or US-09-947-914-75
                                                                      ; ORGANISM: Zem mayo; FEATURE: OTHER INFORMATION: Clone ID: 700331949_FLI US-10-425-114A-3571
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                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Kowalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 21
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 33391
LENGTH: 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3571, Application US/10425114A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33391, Application US/10425114A GENERAL INFORMATION:
   Query Match
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OTHER INFORMATION: Clone ID: UC-ZMFLMO17105A02_FLI-10-425-114A-33391
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Zea mays
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Similarity 80.8%;
21; Conservative
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76.7%;
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Pred. No. 41;
   Score 17.8;
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Length 1189;
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US-10-425-114A-19153
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                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: 700549530_FLI US-10-425-114A-5952
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Sceen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 19153
LENGTH: 1268
TYPE: DNA
OPENIUM. 72-2016
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(553131)B CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NO5: 73128 SEQ ID NO 5952 LENGTH: 1327
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Best Local Similarity 90.5%; Pred. No. 8:
Matches 19; Conservative 0; Mismatche
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Matches 22; Conservative
                                                                                                           Query Match
Best Local Similarity
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
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                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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                                                                                    59.3%; Score 17.8; ilarity 90.5%; Pred. No. 87; Conservative 0; Mismatches
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APPLICANT: Kovalia, David K.

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E

ITITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
INUMBER OF SEQ ID NOS: 73128
SEQ ID NO 1209
LENGTH: 1111
TYPE: nw"
RESULT 9
US-10-428-487-41
US-10-428-487-41; Sequence 41, Application US/10428487; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA K.
; APPLICANT: GERBER, HANS-PETER
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Best Local Similarity
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Best Local :
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LENGTH: 1746
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nuclesic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
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ORGANISM: Zea mays
FEATURE:
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Local Similarity 75.9%;
hes 22; Conservative
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Pred. No. 89;
0; Mismatches
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Pred. No. 1.1e+02;
0; Mismatches 4; Indels 0
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APPLICANT: MONBARTO
APPLICANT: MONBARTO
APPLICANT: MONBARTO
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Soybean Polymorphisms and Methods of
FILE REFERENCE: 38-15 (53382)
CURRENT APPLICATION NUMBER: US/60/480,590
CURRENT FILING DATE: 2003-06-20
NUMBER OF SEQ ID NOS: 6578
SOFTWARE: Patentin version 3.2
SEQ ID NO 5114
LENGTH: 734
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TITLE OF INVENTION: Functional Sites
FILE REFERENCE: 11207-029-228
CURRENT APPLICATION NUMBER: PCT/US03/18714
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/387,887
PRIOR FILING DATE: 2002-06-13
PRIOR PPLICATION NUMBER: US 60/387,910
PRIOR PPLICATION NUMBER: US 60/387,910
PRIOR PILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 51999
SOPTWARE: Patentin version 3.2
SEQ ID NO 21709
LENGTH: 263
TYPE: DATE: 2002-06-13
TYPE: DATE: 2002-06-13
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-428-487-41
; TYPE: DNA; ORGANISM: Glycine max US-60-480-590-5114
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; Sequence 5114, Application US/60480590
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/428,487
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/815,153
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,201
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 84
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Best Local Similarity
Matches 20; Conserv
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SEQ ID NO 41
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Pred. No. 1.1e+(
0; Mismatches
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                                                                                                                ; OTHER INFORMATION: Clone ID: 700241792_FLI US-10-425-114A-3130
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Best Local Similarity
Matches 21; Conserv
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SEQ ID NO 3130
LENGTH: 1647
                                                       Query Match
Best Local S
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ma, Xiao Jun
TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from
TITLE OF INVENTION: ecsinophil cells
FILE REFERENCE: S03157-01
CURRENT APPLICATION NUMBER: US/10/350,923B
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: US/ 09/454,280
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-06-12
PRIOR APPLICATION NUMBER: PCT/US99/28773
PRIOR APPLICATION NUMBER: US/ 60/111,006
                                                                                                                                                                                                                                                              APPLICANT: Zhou, Yīhua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)8
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dotson, Stanton B. APPLICANT: Ma, Xiao Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
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                                                                                                                                                                                         TYPE: DNA
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77.8%;
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                                     Score 17.4; DB 6;
Pred. No. 1.3e+02;
0; Mismatches 6;
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Pred. No. 1.3e+02
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APPLICANT: CARGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
TITLE OF INVENTION: RESPONSE TO INTERFERON
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11874
LENGTH: 100537
TYPE: DNA
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FEATURE:
RAME/KEY: misc feature
LOCATION: (1)...(4813087)
OTHER INFORMATION: n = A,T,C or G
US-09-947-914-75
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US-09-947-914-75/c
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US-60-485-450-11874
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US-60-485-450-11874
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Search completed: September 16, Job time : 67.2277 secs
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM
TITLE OF INVENTION: 21, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001298
CURRENT APPLICATION NUMBER: US/09/947,914
CURRENT FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SEQ ID NO 75
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              LENGTH: 4813087
TYPE: DNA
                                                                           1761296 CCCTGCGTTGGGGAATATCCTCCTGCA 1761270
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Local Similarity 77.8%;
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Pred. No. 1.6e+02;
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##: //GMZ 6/prodata/2/pna/US1016_COMB.seq;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

| 0 1 2 2 4 | Result |
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| 32.6 32.6 31.4 22.6 | Score |
| 98.8 98.8 95.2 | Query Match I |
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| 98.8 33 25 US-09-594-065-4 98.8 33 25 US-09-594-065-10 95.2 33 25 US-09-594-065-11 68.5 39 25 US-09-594-065-7 | SUMMARIES |
| Sequence 4, Appli Sequence 10, Appl Sequence 11, Appl Sequence 7, Appli | Description |

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US-09-594-065-4
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                                                                                                                                                             Sequence 4, Application US/09594065

GENERAL INFORMATION:
APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and Kits for Herpes Simplex Virus Type 1
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 33
TYPE: DNA
TYPE: DNA
                                        Matches
                                                            Query Match
Best Local (
                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
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                                                            Similarity
CCCTGCAAACTCGTGKTCCTCCAGCATGCAGGG
                                              Conservative
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100.0%; Pre
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13 US-09-294-404-78
14 US-08-123-456-217
18 US-09-297-477A-217
18 US-09-297-477A-217
19 US-09-297-477A-211
19 US-09-297-477A-211
19 US-09-297-477A-211
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US-08-940-229-7578
US-60-027-778-144
US-09-540-229-89186
US-09-540-229-100072
US-09-540-229-100072
US-09-540-229-100072
US-09-540-208-1734
US-09-540-208-1734
US-09-540-208-1734
US-09-540-208-1764
US-09-540-208-1764
US-09-933-524-21764
US-09-933-524-21766
US-09-934-956-16027
US-09-934-956-11498
US-10-029-386-11498
US-10-029-386-11498
US-10-029-386-25205
US-09-947-907-2022
US-09-949-016-37689
                                                           Score 32.6; DB 29
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                                              Mismatches
                                                                                                                      96
                                                                                                                      molecular beacon
                                                                         DB 25;
                                                                       Length 33;
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Sequence 141, App
Sequence 141, App
Sequence 78, Appl
Sequence 78, Appl
Sequence 27, App
Sequence 217, App
Sequence 217, App
Sequence 8, Appli
Sequence 1744, Ap
Sequence 1774, Ap
Sequence 21764, A
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Sequence 10, Application US/09594065
GENERAL INFORMATION:
APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and Kil
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT APPLICATION NUMBER: US/09/594,065
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 10
LENGTH: 33
TYPE: DNA
                                                                                                                                           RESULT 4
US-09-594-065-7/c
                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: HSV type-2 US-09-594-065-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-594-065-11
US-09-694-065-11
; Sequence 11, Application US/09594065
; GENERAL INFORMATION:
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US-09-594-065-10
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and Kits for Herpes Simplex Virus Type
TITLE OF INVENTION: Mucleic Acid Detection
FILE REFERENCE: 25436/1280
CURRENT PILION NUMBER: US/09/594,065
CURRENT PILION DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 33
TYPE: DNA
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Matches
                                                                   Sequence 7, Application US/09594065
GENERAL INFORMATION:
APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
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TITLE OF INVENTION: Compositions, methods and TITLE OF INVENTION: Nucleic Acid Detection FILE REFERENCE: 25436/1280 CURRENT APPLICATION NUMBER: US/09/594,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: HSV type-1 specific molecular beacon
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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32; Conserv
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97.0%;
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97.0%;
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Pred. No. 0.0083;
1; Mismatches
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Pred. No. 0.02
0; Mismatches
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US-09-594-065-13/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 13
LENGTH: 109
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                         Sequence 141, Applic GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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Best Local S
SEQ ID
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CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WalkerPeach, Cindy
APPLICANT: DuBois, Dwight
TITLE OF INVENTION: Compositions, methods and Kits for Herpes Simplex Virus Type 1 an
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: 25436/1280
             CURRENT APPLICATION NUMBER: US/08/123,456
CURRENT FILING DATE: 1997-03-03
PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR PILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 303
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                       APPLICANT: DILLON, SUSAN B.
APPLICANT: LEARY, JEFFREY JOSEPH
APPLICANT: SUTTON, DAVID
TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0
                                                                                                                                                              FILE REFERENCE:
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Sequence amplified by PCR for HSV type-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 CAMACTCGTGGTCCTCCAGCATG 38
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DABROWSKI-AMARAL, CHRISTINE ELLEN
                                                                                                                                                                                                                                                                  DELVECCHIO, ALFRED MICHAEL
                                                                                                                                                                                                                                                                                                                                                          Application US/08123456
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95.7%;
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Pred. No. 1.2e+02;
1; Mismatches (
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Pred. No. 1.1e+02;
1; Mismatches 0;
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Best Local Similarity
Watches 22; Conserve
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; TYPB: DNA
; ORGANISM: Herpes simplex
US-08-123-456-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-297-477A-141
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APPLICANT:
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nes 22; Conserv
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FILE REFERENCE: PS0583

CURRENT APPLICATION NUMBER: US/09/297,477A

CURRENT FILING DATE: 1999-66-29

PRIOR APPLICATION NUMBER: US 60/030,279

PRIOR FILING DATE: 1999-11-04

PRIOR FILING DATE: 1999-11-04

PRIOR FILING DATE: 1999-10-04

PRIOR FILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 303

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 141

LENGTH: 2645

TYPE: DNA

ORGANISM: Herpes simplex
APPLICANT: DILLON, SUSAN B.

APPLICANT: LEARY, JEFFREY JOSEPH
APPLICANT: SUTTON, DAVID

TITLE OF INVENTION: NOVEL CODING SEQUENCES FR
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
FILE REFERENCE: P50583
CURRENT APPLICATION NUMBER: US/09/94,404
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/297,477
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 141, Application US/09297477A
GENERAL INFORMATION:
APPLICANT: ESSER, KLAUS M.
APPLICANT: CHAN, JOHN Y.
APPLICANT: DABROWSKI-AMARAL, CHRISTII
APPLICANT: DELVECCHIO, ALFRED MICHAEL
APPLICANT: DELVECCHIO, ALFRED MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 141, Application US/09994404 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                APPLICANT: ESSER, KLAUS M.
APPLICANT: CHAN, JOHN Y.
APPLICANT: DABROWSKI-AMAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SUTTON, DAVID
TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       755 CAAACTCGTGGTCCTCCAGCATG 777
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LEARY, JEFFREY JOSEPH
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Pred. No. 1.8e+02;
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Pred. No. 1.
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                                                                                                                                                                                                                           FROM HERPES
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; ORGANISM: Herpes simplex
US-09-994-404-141
                                                                                                                                                                                                          US-09-297-477A-78/c
; Sequence 78, Application US/09297477A
; GENERAL INFORMATION:
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Best Local Similarity 95.7
Matches 22; Conservative
*CURRENT APPLICATION NUMBER: US/09/297,477A
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SEQ ID NO 141
LENGTH: 2645
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Best Local :
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                                                                       APPLICANT: ESSER, KLAUS M.
APPLICANT: CHAN, JOHN A.
APPLICANT: DABROWSKI-AWARAL, CHRISTINE ELLEN
APPLICANT: DELVECCHIO, ALFRED MICHAEL
APPLICANT: DILLON, SUSAN B.
APPLICANT: LEARY, JEFFRRY JOSEPH
APPLICANT: LEARY, JEFFRRY JOSEPH
APPLICANT: SUTTON, DAVID
                               APPLICANT: DILLON, SUSAN B.
APPLICANT: LEATN, JEFFREY JOSEPH
APPLICANT: SUTTON, DAVID
TITLE OF INVENTION: NOVEL CODING SEQUENCES
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1997-03-03
PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/049,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/123,456
CURRENT FILING DATE: 1997-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SUTTON, DAVID TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
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                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unknown
LOCATION: (2591) (2825) (2833)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Herpes simplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2841
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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DELVECCHIO, ALFRED MICHAEL
DILLON, SUSAN B.
LEARY, JEFFREY JOSEPH
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                     P50583
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95.7%;
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Pred. No. 1.8e+02;
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L.8e+02;
                                                         FROM HERPES
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APPLICANT: LEAK, OFFERDA COURT.

APPLICANT: SUTTON, DAVID

ITITLE OF INVENTION: NOVEL CODING SEQUENCES FROM THE REFERENCE: P50583

CURRENT APPLICATION NUMBER: US/09/994,404

CURRENT FILING DATE: 2001-11-26

PRIOR APPLICATION NUMBER: 09/297,477

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 60/030,279

PRIOR PILING DATE: 1999-11-04

PRIOR PILING DATE: 1999-10-09

PRIOR PILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 303

SOFTWARE: FASTSEQ for Windows Version 3.0

1 SEQ ID NO 78

**EMECTH: 2841
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SEQ ID NO 78
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                                                                                                               Query Match
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                                                                                              Query Match 68.5%; Score 22.6; DB 43; Best Local Similarity 95.7%; Pred. No. 1.8e+02;
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PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ESSER, KLAUS M. APPLICANT: CHAN, JOHN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 303
SOFTWARE: FastSEQ for Windows Version 3.
                                                                                                                                                                                                                                LENGTH: 2841
TYPE: DNA
ORGANISM: Herpes simplex
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: (2591)(2825)(2833)
OTHER INFORMATION: where n can equal A,G,C,T/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2841
TYPE: DNA
                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (2591)(2825)(2833)
OTHER INFORMATION: where n can equal A,G,C,T/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Herpes simplex FEATURE:
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Local Similarity 95.7%;
les 22; Conservative 1
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2071
                      6 CAAACTCGTGKTCCTCCAGCATG 28
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CAAACTCGTGGTCCTCCAGCATG 2049
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LEARY, JEFFREY JOSEPH
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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Pred. No. 1.8e+02;
                                                                              Mismatches
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                                                                                                                 Length 2841;
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RESULT 12 US-08-123-456-217

Sequence 217, Application US/08123456 GENERAL INFORMATION:

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SEQ ID NO 217
 Best Local Similarity Matches 22; Conserv
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                                    Query Match
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                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/297,477A CURRENT FILING DATE: 1999-06-29 PRIOR APPLICATION NUMBER: US 60/030,279 PRIOR FILING DATE: 1999-11-04 PRIOR APPLICATION NUMBER: US 60/049,018 PRIOR APPLICATION NUMBER: US 60/049,018 PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/123,456
CURRENT FILING DATE: 1997-03-03
PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 303
                                                                TYPE: DNA
ORGANISM: Herpes simplex
PRATURE:
NAME/KEY: unsure
LOCATION: (100831) (100832) (100833) (111047) (111050) (111051)
OTHER INFORMATION: where n can equal A,G,C,T/U
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SUTTON, DAVID
TITLE OF INVENTION: NOVEL CODING SEQUENCES
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
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                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Herpes simplex
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                                                                                                                                                                                                     LENGTH: 117213
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LEARY, JEFFREY JOSEPH
SUTTON, DAVID
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LEARY, JEFFREY JOSEPH
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLAUS M.
               68.5%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.5%;
Score 22.6; DB 18;
Pred. No. 2.8e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHRISTINE ELLEN
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Pred. No. 2.8e+02;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                         FROM HERPES
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                                Length 117213;
   Indels
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                                                       PCT-US01-11372-8
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                                                                                                                            PRIOR APPLICATION NUMBER: 60/195,680
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 217, Applic GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application PC/TUS0111372 GENERAL INFORMATION:
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Best Local Similarity
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 Best Local Similarity
                   Query Match
                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: PCT/US01/11372
CURRENT FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                        APPLICANT: KINSEY, BERMA
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: MACRAGEREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION TITLE OF INVENTION: DELIVERY AGENTS
FILE REFERENCE: P01949US1/10004014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/994,404
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/297,477
PRIOR FILING DATE: 1999-06-29.
PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR FILING DATE: 1999-11-04
                                                                                                                                                                                                                                                                                                                         APPLICANT: ORSON, APPLICANT: KINSE BHOGA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/049,018 PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: P50583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL CODING SEQUENCES TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                 LENGTH: 154746
TYPE: DNA
ORGANISM: HERPESVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (100831)(100832)(100833)(111047)(111050)(111051)
LOCATION: (111052)(111053)
OTHER INFORMATION: where n can equal A,G,C,T/U
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| Search completed: September 16, 2003, 22:44:57 Job time : 2395.32 secs | 54077 CAAACTCGTGGTCCTCCAGCATG 54099 | 6 CAPACTCGTGKTCCTCCAGCATG 28 | Matches 22; Conservative |
| 2003 | AGCAT | AGCAT | 1, |
| , 22:44:57 | G 54099 | G 28 | 1; Mismatches |
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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// cgn2_6/ptcdata/2/pna/US06_NEW_COMB.seq:*

// cgn2_6/ptcdata/2/pna/US07_NEW_COMB.seq:*

// cgn2_6/ptcdata/2/pna/US08_NEW_COMB.seq:*

// cgn2_6/ptcdata/2/pna/US08_NEW_COMB.seq:*

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US-99-998-576-24
US-9-998-576-24
US-60-495-114-16801
US-60-487-610-19824
US-60-487-610-19824
US-60-487-610-19824
US-60-485-114-16591
US-60-495-114-16591
US-60-495-114-3169
US-60-495-114-3169
US-60-493-007-3356
PCT-US03-07340B-10
US-60-485-450-121181
PCT-US03-07340B-10
US-60-485-450-121181
PCT-US03-07340B-10
US-60-485-450-12181
PCT-US03-516A-33653
US-09-897-516A-3853
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US-60-490-890-2277
US-60-487-610-19291
US-60-487-610-19887
5 US-09-947-914-75
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535.803 Million cell updates/sec
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Sequence 75, Appl
Sequence 3124, Ap
Sequence 1136, Ap
Sequence 16801, A
Sequence 19825, A
Sequence 12335, A
Sequence 12207, A
Sequence 16591, A
Sequence 16591, A
Sequence 30109, A
Sequence 30109, A
Sequence 19737, A
Sequence 11737, A
Sequence 11737, A
Sequence 3356, Ap
Sequence 34704, A
Sequence 12181, Appl
Sequence 423, App
Sequence 423, App
Sequence 3852, Ap
Sequence 3853, Ap
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Sequence 19291, A
Sequence 19887, A
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| 56.4 | 56.4 | 56.4 | 56.4 | 56.4 | 56.4 | 56.4 | 56.4 | | 56.4 | | | 56.4 | 56.4 | 56.4 | 56.4 | | 56.4 | |
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| | Sequence | aprianhae |
| 3872, | 3871, | 3870, | 3869, | 3868, | 3867, | 3866, | 3865, | 3864, | 3863, | 3862, | 3861, | 3860, | 3859, | 3858, | 3857, | 3856, | 3855, | 0004 |
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ALIGNMENTS

US-60-496-393-1/c ; Sequence 1, Application US/60496393 ; GENERAL INFORMATION:

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Sequence 30, Application PC/TUS0321510

GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
ITITLE OF INVENTION: MP21S AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX03-046C-PC
CURRENT APPLICATION NUMBER: PCT/US03/21510
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 60/394,795
PRIOR APPLICATION NUMBER: US 60/401,739
PRIOR APPLICATION NUMBER: US 50/401,739
PRIOR APPLICATION NUMBER: US 60/411,010
PRIOR APPLICATION NUMBER: US 60/411,010
PRIOR FILING DATE: 2002-08-07
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-12-30
NUMBER OF SEO ID NOS: 124
SOFTWARE: PATENTIN VETSION 3.2
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-496-393-1
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CURRENT FILING DATE: 2003-08-20
NUMBER OF SEQ ID NOS: 40
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APPLICANT: Yakir , Liat
APPLICANT: Yarden, Yosef
TITLE OF INVENTION: TREATING TSG101-ASSOCIATED DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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22; Conserv
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Pred. No. 2
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APPLICANT: Rupnow, Brent A.

APPLICANT: Webster, Kevin R.

APPLICANT: Webster, Kevin R.

APPLICANT: Wong, Tai W.

TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION PSILE REFERENCE: D0310 PSP:

CURRENT APPLICATION NUMBER: US/60/490,890

CURRENT PILING DATE: 2003-07-29

NUMBER OF SEQ ID NOS: 2779

SOOPTWARE: PatentIn version 3.2

TYPE: DN^

TYPE: DN^
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; SEQ ID NO 19291
; LENGTH: 36377
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-19291
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PCT-US03-21510-30
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                                                          Best Local Similarity
Matches 23; Conserv
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APPLICANT: HUNG, HONG!IN
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-I
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
                                                                                                                                                                                                                                                                           FILE REFERENCE: CL001469
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Local Similarity 75.8%;
les 25; Conservative
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                               N
                              CCTGCAAACTCGTGKTCCTCCAGCATGCAG 31
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                                                             Conservative
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75.8%;
                                                                             60.6%;
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                                                            1; Mismatches
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Pred. No. 24;
                                                                             Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20.2;
Pred. No. 24;
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                                                                             DB 7;
                                                                                                                                                                                                                                                                                       AND USES THEREOF
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                                                                                            Length 36377;
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                                                             Gaps
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; LENGTH: 4813087
; TYPE: DNA
; ORGANISM: HUMAN
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4813087)
; OTHER INFORMATION: n = A,T,C or G
US-09-947-914-75
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HIDANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIRROSIS IN HEPATITIS C VIRUS-INFECTITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEG ID NOS: 97101
SOPTWARE: PASESEQ for Windows Version 4.0
15007114687
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US-09-947-914-75/c
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; ORGANISM: Homo sapiens
US-60-487-610-19887
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                                                                                                                                                                                                                                                                                              US-60-493-007-3124/c
APPLICANT: Johnson, No.;
APPLICANT: Higgs, Brandon
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Primary rat hepatocyte toxicity modeling
FILE REFERENCE: 44921-5113-01-US
CURRENT APPLICATION NUMBER: US/60/493,007
CURRENT APPLICATION NUMBER: US/60/493,007
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SEQ ID NO 75
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Best Local Similarity 76.7
23; Conservative
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM
TITLE OF INVENTION: 21, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001298
CURRENT APPLICATION NUMBER: US/09/947,914
CURRENT FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                            Sequence 3124, Application US/60493007
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                         APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
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                                                                                                                                                                                                                                                                                                                                                                                    3040475 CCCTGCACCCTGGGGTAGCTCCAGCATGCA 3040446
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76.7%;
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Pred. No. 74;
l; Mismatches
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RESULT 9
US-09-084-576-244/c
; Sequence 244, Application US/09908576; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 97101
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1136
LENGTH: 904
TYPE: DNA
CRGANISM: Homo sapiens
US-60-487-610-1136
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US-60-487-610-1136
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                                                                                                                                                                                     Matches
                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CARGILL, Michele
APPLICANT: HUANG, HONGJIN
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/60/487,610 CURRENT FILING DATE: 2003-07-17
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PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/374,139
PRIOR FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US 60/394,253
PRIOR FILING DATE: 2002-07-09
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TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/371,150 FILING DATE: 2002-04-10 APPLICATION NUMBER: US 60/371,413 FILING DATE: 2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/370,248 FILING DATE: 2002-04-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/371,135 FILING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2002-03-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107
                                                                                                           782 CCCTGCACTCCCAGTTGTTCCAGCATTCTGGG
                                                                                                                                               1 CCCTGCAAACTCGTGKTCCTCCAGCATGCAGGG 33
                                                                                                                                                                                  ch 60.0%; Similarity 72.7%; 24; Conservative
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Pred. No. 29;
1; Mismatches
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Pred. No. 29;
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; SEQ ID NO 244
; LENGTH: 3679
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-908-576-244
RESULT 10
US-60-495-114-16801
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                                                                                                                                             Matches
                                                                                                                                                                              Query Match
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PRIOR FILING DATE: 1999-10-05
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 423
                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/09/665,350B
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/09/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US/09/143,048
PRIOR FILING DATE: 1999-07-07
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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CURRENT APPLICATION NUMBER: US/09/908,576
CURRENT FILING DATE: 2001-07-18
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 69/146,222
PRIOR FILING DATE: 1999-07-28
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                                                                                                                                                               Local
                                                                       1297
                                                                                                                                             Similarity
21; Conserv
                                                                         CCCTGCAAAGCTGTGGTCCTCCAGC 1273
                                                                                                        cccrecaaacrcerekrccrccaec 25
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Ashkenazi, Avi
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher
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Filvaroff, Ellen
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Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desnoyers, Luc
                                                                                                                                             Conservative
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                                                                                                                                                          60.0%;
84.0%;
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                                                                                                                                         Score 19.8; D
Pred. No. 37;
1; Mismatches
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                                                                                                                                                                            DB 5;
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                                                                                                                                                                            Length 3679;
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                                                                                                                                         Gaps
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Sequence 16801, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES

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Sequence 12335, Application US/60485450

GENERAL INFORMATION:
APPLICANT: CHARGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPP
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SRO ID NOS: 47859
SOFTWARE: PASTSEQ for Windows Version 4.0
EEQ ID NO 12335
LENGTH: 29102
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                                                                                                                                                                                                                                                                                                           RESULT 12
US-60-485-450-12335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-19825
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CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTMARE: FRACSEQ for Windows Version 4.0
SEQ ID NO 16801
LENGTH: 26000
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LENGTH: 29102
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-I
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1469
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FRANCSEQ for Windows Version 4.0
TYPE: DNA
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TITLE OF INVENTION: USE
FILE REFERENCE: CL001480
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FEATURE:
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(26000)
OTHER INFORMATION: n = A,T,C or G,
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72.7%;
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Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.8;
Pred. No. 51;
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DETECTION
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APPLICANT: CARGILL, Michele

APPLICANT: CHANG, Sheng-Yung

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEP-

TITLE OF INVENTION: THREOF

TITLE OF INVENTION: THEROF

FILE REFERENCE: CL001470

CURRENT APPLICATION NUMBER: US/60/485,450

CURRENT FILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 47859

SOFTWARE: FASTSEQ for Windows Version 4.0

1. SEC ID NO 12207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-60-487-610-19824/c
US-60-487-610-19824/c
Sequence 19824, Application US/60487610
GENERAL INFORMATION:
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                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-485-450-12207
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US-60-485-450-12207/c
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US-60-485-450-12335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongiin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 19824
LENGTH: 60476
                                                                  Query Match 60.0%;
Best Local Similarity 72.7%;
Matches 24; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                              ENGTH: 60476
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nes 24; Conservative
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58060
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CCCTGCACTCTCCAGTTGTTCCAGCATTCTGGG 58028
                               CCCTGCAAACTCGTGKTCCTCCAGCATGCAGGG
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72.7%;
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Pred. No. 51;
1; Mismatches
                                                                  Score 19.8; D
Pred. No. 58;
1; Mismatches
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Pred. No. 58
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RESULT 15 US-60-495-114-16591/c

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Sequence 16591, Application US/60495114

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLB OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLB OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
TITLB OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
CURRENT PPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16591
LENGTH: 62312
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(62312)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-60-495-114-16591
Search completed: September 16, 2003, 22:48:21 Job time: 59.9505 Becs
                                                                                                           밁
                                                                                                                                                                                                      Query Match 60.0%; Score 19.8; DB 7; Length 62312; Best Local Similarity 72.7%; Pred. No. 58; Matches 24; Conservative 1; Mismatches 8; Indels 0;
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BEST AVAILABLE COPY

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length: 2000000000
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            2888711 seqs, 20454813386 residues
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Pred. No.

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| RESULT 1 103657/c LOCUS DEPINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL | | 44 | 44 | . 4. | w د | ww | ωι | | | 0 0 331 | N | งง | NN | 0 10 1 | งง | NN | , | . بر د | | <u> </u> | . سر ه | | | | | | 0 3 2 | c 1 | Result No. |
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| e 5 cgic s; ifie | | 9.9 | 00. | | 9.0 | 000 | | 999 | • | ŌĊ | | • | 00 | | | ° ° | | 0 | 00 | | .0 | | | 9 | | .0 | 00.0 | Ō | Query Match Le |
| from Pa [::2686] 1. 798 to 798 to 798 1 B of 1 B of | | | | | | | | | | 3465 | | | | | | | | | | | | | | | | | | | ngth D |
| itent U | | E 00 | 6 E03 | EOS | A. SH. | 4 . 10g | HS HS | | | 6 803 | | 4 | 4 | | | 44 | 4 4 | 4. | 44 | 44 | 4. | 4 | | | | 4 | 14 S7 | 10 | a, in |
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/db_xref="taxon:10298"
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Original source text: HSV1 strain tsB5 DNA, clone pTBG-BS1.
HSV1 strain tsB5 is a mutant of strain HFEM that is temperature dependent for virus growth, production of gB, and fusion of Vero and HBL cells. The syn and ts lesions of tsB5 are separable by recombination, the syn defect being located between 0.345 and 0.355 map units, and the ts defect being located between 0.360 and 0.368 map units. The rate of entry determinant of tsB5 is genetically separable from both the syn and ts lesions and is located between 0.350 and 0.360 map units, which is entirely within the glycoprotein B gene (0.348 to 0.366 map units).
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J. Virol. 67 (10), 5948-5954 (1993)
93381796
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Bzik, D.J., Fox, B.A., DeLuca, N.A. and Person, S.
Nucleotide sequence of a region of the harpes simplex virus type 1
gB glycoprotein gene: mutations affecting rate of virus entry and
                                                                                                                                                                                                                                                                                                                       Virology 137 (1), 185-190 (1984) 84301857
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/protein_id="AAP13961.1"
/db_xref="GI:30027723"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpesviridae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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SOURCE
ORGANISM
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AUTHORS
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ACCESSION
VERSION
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E03093/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
     AL PATENT: JP 191218397-A 2 25-SEP-1991;

TAKEDA CHEM IND LTD

OS Herpes simplex virus type1 (HSV-1)

PN JP 191218397-A/2

PN JP 191218397-A/2

PP 21-JUN-1990 JP 1990161448

PR 22-JUN-1989 JP 89P 158238, 30-NOV-1989 JP 89P 308941 PI

FUJISAWA YUKIO, HINUMA KUNIJI, ASAKAWA NAOKI, OTAKA SACHIKO PC

CO7K13/00,C12N1/19,C12N15/38,C12P21/02//A61K39/245,(C12N1/19, PC

C12R1:865),

PC (C12P21/02,C12R1:865);

CC topology: Linear;

CC typothetical: No;

CC *Source: strain=Miyama;

CC *source: strain=Miyama;

FH Key Location/Qualifiers
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DNA encoding truncated gB of herpes simplex virus typel(HSV-1).
E03093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human herpesvirus 1
Human herpesvirus 1
Viruses, dadNa viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 2088)
Pujisawa; Y., Hinuma, K., Asakawa, N. and Otaka, S.
POLYPEPTIDE AND ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stain ts85 has a total of 12 base substitutions within the coding region for 9B when compared to strain KOS. Of these, only two cause amino acid substitutions, a 't' to 'c' transition at bp 695 causes a Val to Ala substitution, and a 'g' to 'a' transition at bp 1610 causes an Arg to His substitution. Because the rate-of-entry determinant has been mapped to between 0.350 and 0.360 mag units, the transition at bp 695 must be responsible for the difference in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B03093.1 GI:2171311 JP 1991218397-A/2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n 100.0%; Score 18; DB 14; Similarity 100.0%; Pred. No. 2.8e+02; 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCAGGCCGCTGTCCTTG 1119
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*source: clone=pHSB106 delta Tth;
*source: clone=pHSB106 delta Tth;
Kev
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I FARRYNATHIKVGQPQYYLANGGFLIAYQPLLSNTLAELYNEEHLREQSRKEPNPTP
PPPGASANAS VERIKTTSS I EFARLQFTYNHIQRHVDMLGRVAIAWCELQNHELTLW
MEARKLAPNAIASATVGRRVSARMLGDVWAVSTCVPVAADNVIVQNSWEISSREPGACY
SRPLVSFRYEDQGPLVEGQLGENNELRLTRDAIEPCTVGHRRYFTFGGGYVYFEEYAY
SHQLSRADITTWSTFIDLNITMLEDHEEVPLEVYTRHEIKDGGYEVFUORTROQRROLHD
LRFADIDTVILHDADANAMPAGIGAFPEGWGDLGRAVGKYWNGIVGGVSSFM
SNPFGALAVGILVLAGLAAAFFAFRYVERLQSNPMKALYPLTTKELKNPTNPDASGEG
EEGGDEDEAKLAEARBMIRYMALVSAMEHTEHKAKKKGTSRLLSAKVTDMVMRKKRNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAA45777.1"
/db_xref="GI:330088"
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|mol_type="genomic DNA"
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of Sall site; map coordinate 0.360.
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ORGANISM
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E00358/c
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KEYWORDS
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                                                                 Local Similarity
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2025
                                                                                                                                                                                                                  Patent: JP 1985115529-A 2 22-JUN-1985;
SUTANREE PAASON
OS helpes simplex virus type 2
PN JP 1985115529-A/2
PN JP 198515529-A/2
PN JP 1985115529-A/2
PN JP 1984129915
PF 23-JUN-1983 US 83 506986, 16-SEP-
SUTANREE PAASON
PC 1861X39/245,C07H21/04,C07K15/14,C12N1
Strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC topology: Linear;
CC *source: strain=HG 52;
CC *source: strain=HG 52;
CC *source: strain=HG 52;
CC *source: strain=HG 52;
FH Key Location/Qualifiers
FH Key Location/Qualifiers
FT CDS .1.2727
PT CDS .1.2727
                                                     18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON-GLYCOSYLATED AMINO ACID CHAIN IMMUNOLOGICALLY REACTIVE TO GLYCOPROTEIN OF HERPES VIRUS 1 AND 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B00358.1 GI:2168645 JP 1985115529-A/2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding glycoprotein B of herpes simplex virus type 2
              AGCAGGCCGCTGTCCTTG 18
AGCAGGCCGCTGTCCTTG 2008
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                                                     Conservative
                                                                                                                                                                                                                                                             *source: clone=p52BXX;
*source: map_position=0.386-0.348;
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           A61K39/245,C07H21/04,C07K15/14,C12N15/00//C12P21/02; CC
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                                                                                                                                                                                     /product='glycoprotein B of herpes simplex virus type 2'.
Location/Qualifiers
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                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:32644"
886 c 841 g 3
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/db_xref="taxon:10298"
751 c 620 g
                                                                                                                                                                organism="unidentified"
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/product='truncated
                                                                 Score 18; DB 6;
Pred. No. 2.8e+02;
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                                                     Mismatches
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                                                                              Length 2586;
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                                                     indels
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FEATURES
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ORGANISM
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AUTHORS
TITLE
JOURNAL
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BD145144/c
LOCUS
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ACCESSION
VERSION
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BD165793/c
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bource
                                             NCE 1 (bases 1 to 2712)

ORS Burke,R.L., Pachl,C. and Valenzuela,P.D.T.

E Vaccine for use in the therapeutic treatment of HSV

PARTICLE PACHICAL PRODUCTIONS

NAL Patent: JP 2002167398-A 2 11-JUN-2002;

OS Herpes simplex virus 7

PN JP 2002167398-A/2

PP 11-JUN-2002

PF 12-SEP-2001 JP 2001277340

PR 20-OCT-1986 US 921.213

PI RAE LYN BURKE,CAROL PACHL, PABLO D T VALENZUELA PC

C07K14/035,A61K39/245,A61P31/22,C12N15/09,C12N15/00, PC

C12N15/00

CC Vaccine for use in the phanone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LL Patent: JP 2002136297-A 4 14-MAY-2002;
CHIRON CORP
OS HSV 981
PN JP 2002136297-A/4
PN JP 2002136297-A/4
PD 14-MAY-2002
PP 10-SEP-2001 JP 2001274335
PR 02-AUG-1990 US 561.528
PI RAE LYN BURKE, ROSE E SEKULOVICH
PC C12N15/09, A61K38/00, A61K39/245, A61P31/12, C07K14/03, C12N15/00, PC A61K37/02
CC Herpes simplex virus VP16 vaccine
FH Key
FT CDS (1): (2712).
                                                                                                                                                                                                                                                                                                                                                                                                                          2096
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Herpes simplex virus VP16 vaccine.
BD14514
BD145144.1 GI:27850902
JP 2002136297-A/4.
                                                                                                                                                                                                                                                       Herpes simplex virus 7
Herpes simplex virus 7
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                               Vaccine for use in the t
BD165793
BD165793.1 GI:27871605
JP 2002167398.A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 2712)
Burke, R.L. and Sekulovich, R.E.
Herpes simplex virus VP16 vaccine
Patent: JP 2002136297-A 4 14-MAY-2002;
                         召
                                                                                                                                                                                                                                                                                                                                                       BD165793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  513
                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Location/Qualifiers CDS (1) .(2712).

Location/Qualifiers
                                    Vaccine for use in the therapeutic Location/Qualifiers
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       (1)..(2712).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
_949 c 853 g 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 18; DB 6;
100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                           the therapeutic treatment
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nt of HS
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                                                              ACCESSION
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SOURCE
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BD145143/c
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BD165795/c
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source
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1 (bases 1 to 2712)

10RS Burke, R.L., Pachl, C. and Valenzuela, P.D.T.

E Vaccine for use in the therapeuric treatment of HSV Patent: JP 2002167398-A 4 11-JUN-2002;

NAL PATENT CORP

OS Herpes simplex virus 7

PN JP 2002167398-A/4

PD 11-JUN-2002

PF 12-SEP-2001 JP 2001277340

PR 20-OCT-1986 US 921.213

PI RAE LYN BURKE, CAROL PACHL, PABLO D T VALENZUELA PC C12N15/00

CC Vaccine for use in the therapeuric reversely.
                                                                                                                                            2715 bp
Herpes simplex virus VP16 vaccine.
Bp145143
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Herpes simplex virus 7
Viruses; dabNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 2715)
Burke,R.L. and Sekulovich,R.E.
Herpes simplex virus VP16 vaccine
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JP 2002167398-A/4.
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                                                     unclassified
                                                                           unidentified
                                                                                                         BD145143.1 GI:27850901
JP 2002136297-A/3.
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larity 100.0%; Pred. No. 2.
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Herpes simplex virus
/mal_type="genomic DNA"
/mal_type="genomic DNA"
/db_xref="texon:57277"
/db_xref="texon:57277"
_949 c 853 g 396 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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MEDLINE
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CHIRON CORP
OS HSV 9B2
PN JP 2002
PD 14-MAY-
PF 10-SEP-
PR 02-AUG-
PI RAE LYN
PC C12N15/
PC A61K37/
CC Herpes
FH Key
FT CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                      Submitted (02-OCT-1998) Institute of Virology, Slovak Academy of Sciences, Dubravska cesta 9, Bratislava 842 46, Slovakia Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human herpesvirus
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AF097023
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Human herpesvirus 1 strain HSZP glycoprotein B.(UL27) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                Herpes simplex virus 1 (HSV-1) strain HSZP glycoprotein B gene: comparison of mutations among strains differing in virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 2715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human herpesvirus 1
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                                                                                                                                                                                                                                                                                                                                                                                                    Virus Genes 20 (1), 27-33 (2000)
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JP 2002136297-A/3
14-MAY-2002
10-SEP-2001 JP 2001274335
02-AUG-1990 US 561.528
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C12N15/09, A61K38/00, A61K39/245, A61P31/12, C07K14/03, C12N15/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus VP16 vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="y=10001:32644"
/db_xref="taxon:32644"
938 c 886 g
                                                                                                                                                                    /db_
                                                                              and cell membrane"
                                                                                       /gene="UL27"
/function="essential for fusion between virion envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
/product="glycoprotein B"
/protein_id="AAF04615.1"
/db_xref="GI:6165612"
                                                            note="envelope glycoprotein; gB"
                                                                                                                                                                                         /organism="Human herpesvirus
/mol_type="genomic DNA"
/strain="HSZP"
                                              codon_start=1
                                                                                                                                            'gene="UL27"
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                                                                                                                             .2715
                                                                                                                                                                          _xref="taxon:10298"
                                                                                                                                                                                                                                                                                                                                   Vojvodova, A., Oravcova, I., Majorova, J., Kudelova, M
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Pred. No. 2.7e+02;
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AF295528/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human herpesvirus 2 glycoprotein B2 (gB2) mRNA, complete cds AF295528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-AUG-2000) Department of Biology, Konkuk University, 1 Hwayang-dong, Kwangjin-gu, Seoul 143-701, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee, H.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human herpesvirus 2
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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                                                                                                                                                                                                                         /gene="gB2"
/codon_start=1
/product="glycoprotein_B2"
/protein_id="AAK97852.1"
/db_xref="gI:15428576"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /moi_type- ..
/strain="G"
                                        / translation="MRGGGLICALVVGALVAAVASAAPAAPRASGGVAATVAANG
GPASRRPPV959ATTKARKKRKKPPRRPEATPPDANATVAAHATLAALLREIKVE
NADAQFYVCPPPTGATVVQFEQPRKCPTRPEGQNYTEGIAVVFKENIA PKYEKAINYE
NADAQFYVCPPPTGATVVQFEQPRKCPTRPEGQNYTEGIAVVFKENIA PKYEKAINYE
KDVTYSQVMPGHRYSQPMGLIEDRAPVPFEBVIDKINAKGVCRSTAKYVRNNMETTAF
KDVTYSQVMPGHRYSQPMGLIEDRAPVPFEBVIDKINAKGVCRSTAKYVRNNMETTAF
HRDDHSTDMELKPAKVATRTSRGMHTTDLKYNPSRVBAFHRYGTTVNCLVEBVDARSV
YPYDBEVLATGDFVYNSPSYVSTEGSHTEHTSYAADRFQVDGFYARDLTTKARATSG
YFRULLTTPKFTVANDMVPKRPAVCTMTKMQEVDENLRAEYGGSFRFSSDAISTTFTT
TRANLTTPKFTVANDMVPKRPAVCTMTKMQEVDENLRAEYGGSFRFSSDAISTTFTT
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RATAPTTRULLTPKFYVANDWYFKSVCTMYKOGEVDEMLESEYGGSFRFSSDAIS
TTFTMLTBKPLSRVLLGDCIGKDARDSVDAIL FARRYNATHI KVGQPQYYLANGGFLI
AYOPLLSNTLAELYVREHLREQSRKPPNPTPPPPGASANASVERIKTTSS I EFARLOF
TYNHI CRHVNDMLGRVA I AWCELQNHELTLMBEARKLANPNA I ASATVGRRVSARNLGD
VMAVSTCVPVAADNVL VOOLSMAISSRPGACYSERLVSFR YEDOGEPLVEGOLGENNELL
LTRDAIEPCTVGHRRYFTFGGGYVYFEEYAYSHQLSRADITTVSTFIDLNITMLEDHE
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GMGDLGAAVGKVVMGIVGGVVSAVSGVSSFMSNEFGALAVGLLVALLVGLLVALAVFAFRSYV
MRLQSNPMKALYPLTYKELKNPTNPDASGEGEBEGGDFDEAKLAARAENAR RYMALVSAM
EHTEHKAKKKGTSALLSAKVTDMVMRKRRNTNYTQVPNKDGDADEDDL"
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ATMYYKDVTVSQVWFGHRYSQFMGIFEDRAPVPFEEVIDKINAKGVCRSTAKYVRNNL
ETTAFHRDDHETDMELKPANAATRTSRGWHTTDLKYNPSRVEAFHRYGTTVNCIVEEV
NLTQYSLSRVDLGDCI GRDAREA I DRMFARKYNATHI KVGQPQYYLATGGFLI A YQPL
LSNTLAELYVREYMREQDRKPRNATPA PLREAPSANAS VER I KTTSS I EFARLQFTYN
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QAANGGPATPAPPALGAAPTGDPKPKKNKKPKNPTPPRPAGDNATVAAGHATLREHLR
                                                                                                                                                                                                                                                                                                                                                             /gene="gB2"
|. .2715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Human herpesvirus 2"
/mol_type="mRNA"
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|. .2715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-OCT-2000) Microbiology-Immunology, Northwestern University Medical School, 320 E. Superior Ave., Ward 6-241, Chicago, IL 60611, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human herpesvirus 1 strain KOS c
AP311740
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Pertel, P.B., Fridberg, A., Parish, M.L. and Spear, P.G.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 279 (1),
21066717
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Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 2715)
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                                                                       QAANGGPATPA PALGÂA PTÖDPKPKKNKKPKNPT PRRAGDNATVAAGHATLREHLR
DI KAERTDANEY VC PEPTGATVOQ EQPRECEPTS PEGQNYTEGI A VVEKENI A PYKEK
ATMY KOLVTYSQ VWEGHEN YG DEGYMEI FEBRA PVP PEEL VIDKI NAKOCHSTAKY VENNL
ETTA FHRDDHETDMEL KPANAATRIS RGWHTTDLKYNPSR VEA FHR YGTTVNCI VEEV
DARS VY PYDEFVLATGDFVYMS PFYGYNEGSHTEHTTY XADAR PKQODGFY ARDLITKA
RATAPTTRULTTE KEFTYAMWVPKR BEVCTYMKWOGS VERMLAGFYK YLANGGFLI
RYQPLLSNTLAEL YVEEHLREGSR KPENFT PP PEGASANAS VER I KYTSSI EFARLOF
TYNHI JOHNNOMLGRVA I AWCELONHELI TLANEAKLAPNA I ASTYDGRV SARWLGD
VMAVSTCV PVAADNVI VQNSME I SSR PCACYSR PLVS FRYEDQGFLVEGQLGERNELR
LTRDA I EPCTYGHRKYETFGGGYVY FEBYA YSHQLSRADI TTVS TE DILNI TMLEDHE
FVPLEVYTRHE I KDSGLLDYTEVQRRNQLADLR RYMALOSLAAF PA FRYV
MRLOSNEMKALY PLTIKELKUPLANSAGEGEGGGDFGAKLARAR FYMAL VSAM
MRLOSNEMKALY PLTIKELKUPLANSAGEGEGGGDFGAKLARAR FRARYV
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DALEPCTVGHRRYFIFGGGYVYFEEYA KSHQLSRADVTTVSTFIDLNITWLEDHBIVP
LEVYTRHEIKDSGLLDYTEVQRRNQLHDLFRADIDTVIRADANAMFAGLCAFFEGMG
DLGRAVCKVMGYVGGVVSAVSGYSSFMSNFFGALAVGLLVLAGIJVAAFFAFRYVLQL
QRNPMKALYPLTTKELKTSDPGGVGGEGEEGAEGGFDEAKLAEAREMIRYMALVSAM
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1939 c 886 g 398 t
                                                      ERTEHKAKKKGTSALLSAKVTDMVMRKRRNTNYTQVPNKDGDADEDDL*
                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MHQGAPSWGRRWFVVWALLGLTLGVLVASAAPSSPGTPGVAAAT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="glycoprotein B"
/protein_id="AAG34116.1"
/db_xref="GI:11321323"
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1 (bases 1 to 2715)

Holland, T.C. and Saharkhiz-Langroodi, A.
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                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-FEB-1996) Dept. of Immunology and Microbiology, Wayne State University, 540 E. Canfield Ave., Detroit, MI 48201, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                               AGCAGGCCGCTGTCCTTG 2082
                                                                                                         AGCAGGCCGCTGTCCTTG 18
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9 951 c 854 g 397 t
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LTRDAIEPCTVGHRRYFTFGGGYVYFEEYAYSHQLSRADITTVSTFIDLNITMLEDHE
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100.0%; Pred. No. 2.7e+02;
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VRL 16-MAY-2000

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AUTHORS
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Search completed: September 16, 2003, 19:14:13 Job time: 395.752 secs
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Best Local Similarity
Matches 18; Conserv
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Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
Direct Submission
Submitted (24-APR-2000) Ophthalmology, Mail Slot 523, University of
Arkansas for Medical Sciences, 4301 West Markham, Little Rock, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 2809)
Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
A viral genetic element involved in a rabbit model of herpes
simplex virus-induced epileptiform seizures
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Human herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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AF259899
AF259899.1 GI:7839508
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tive 0; Mismatches 0;
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd
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ABX17925
                                                                                                                                                                                                      AAV81738
AAS03164
                                                                                                                                                                                                                                                                                        ABX15341
AAV44840
                                                                                  AAV44826
                                                                                                                                                                                     ABL12221
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AAN(60195 AAN(706471 AAQ(14478) AAT93650 AAN(80907) AAQ(8497) AAQ(8497) AAQ(8497) AAQ(8497) AAN(80908) AAN(80908)

cDNA encoding rabb Rabbit progesteron PhCMV*-1 rabbit pr

Pseudomonas aerugi PhCMV*-1 promoter PhCMV*-1-controlle

Rabbit progesteron
Rabbit progesteron
Rabbit progesteron
Clone related to F
Human immune/haema
Nucleotide sequenc
Sphingomonas sp. s
Sphingomonas desul

Human monocyte inh
Human monocyte inh
PCR-III coding seq
Lung cancer relate

Human macrophage-e DNA encoding novel Drosophila melanog

Human monocyte inh DNA encoding human Human NOV27a CG938

Herpes simplex vir Sequence of Herpes DNA fragment encod Sequence encoding HSV-2 strain SB5 C Human herpesvirus

HSVgB gene. Herpe Herpes simplex vir Sequence of Herpes Herpes simplex vir Recombinant herpes

Glycoprotein B (gB Glycoprotein B (gB

ALIGNMENTS

AAQ14479 standard; DNA; 2088 Vaccine; antigen; ss. Herpes simplex virus. Truncated HSVgB gene. (TAKE) TAKEDA CHEM IND LTD (updated)
(first entry) 89JP-0308941. 89JP-0158238. 90JP-0161448. 90JP-0161448 Location/Qualifiers /*tag= a 1..2088 BP.

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RESULT 2
AAV62158
AID AAV6
XX AAV6
AC AAV6
XX AAV6
XX AAV6
XX HSV-
XX HSV-
XX HSV-
XX HSV-
XX HSV-
XX HOPE
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PT And
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XX CLar
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence encodes a truncated form of the HSVgB polypeptide. The recombinant protein can be used to prepare vaccines for prophylaxis of HSV infection and for use in diagnostic kits. See also AAQ14478.
                                                                                                                                                                                                   Chan
           This sequence represents a Herpes simplex virus type-2 (HSV-2) DN sequence of the invention. This sequence was isolated from HSV-2 SB5 (deposited as ATCC VR-2546), is designated Contig ID 14, and a HSV-2 protein. The protein can be used for the treatment or
                                                                          Claim 1;
                                                                                                             Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in
                                                                                                                                                               WPI; 1998-286847/25
                                                                                                                                                                                                                                                     09-JUN-1997;
04-NOV-1996;
                                                                                                                                                                                                                                                                                          31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV62158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2088 BP; 417 A; 751 C; 620 G; 300 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 7; 24pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cheaply and safely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSVgB polypeptide(s) obtd.
useful as vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-328397/45
P-PSDB; AAR14666.
                                                                                                                                                                                                                                                                                                                  14-MAY-1998
                                                                                                                                                                                                                                                                                                                                         WO9820016-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSV-2
                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2012
                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain SB5; immunole iral identification;
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                                                                                                                                                                                                                                                                                                                                                                                                                               simplex virus type
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAGGCCGCTGTCCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on 25-MAR-2003 to correct PA field.)
                                                                         Page 406-407; 748pp; English
                                                                                                                                                                                      Dabrowski-Amaral CE,
Leary JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                     97US-0049018.
96US-0030279.
                                                                                                                                                                                                                                                                                          97WO-US20016
                                                                                                                                                                                                                                                                                                                                                                                         complement (81..2645)
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contig ID 14 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunological ication; viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                <u>د</u>
                                                                                                                                                                                                                                                                                                                                                                "ORF#1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by recombinant DNA techniques HSV and in diagnosis, can be |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995
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Pred. No.
                                                                                                                                                                                                   Delvecchio AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy;
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AGCAGGCCGCTGTCCTTG

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AAN71303/c
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Best Local S
Matches 18
                                         Best
                              Matches
                                                  Query Match
                                                                                           A pure non-glycosylated amino acid (AA) chain comprising a sequence corresponding to that occurring in glycoprotein B of HSV-1 or HSV-2 virus which is antigenic to HSV-1 of HSV-2, which contains no more than 750 AA residues, and which includes AA residues 135-649 inclusive is claimed. It can be used to produce vaccines for prophylaxis and treatment of HSV-1 and HSV-2. See AAN71399 for the HSV-2 sequence.

(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological
                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine; prophylaxis; glycoprotein; gB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAN71303;
                                                                         Sequence
                                                                                                                                                                                            Example;
                                                                                                                                                                                                                                                                      WPI; 1987-056354/08.
                                                                                                                                                                                                                                                                                                                                                          20-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                     US4642333-A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herpes Simplex Virus-1 gB from pKBXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
30-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                            recombinant and used
                                                                                                                                                                                                                                      Amino
                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                           Person
                                                                                                                                                                                                                                                                                                                                      20-JUN-1984;
                                                                                                                                                                                                                                                                                                                 (PERS/) PERSON
                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            706
                                                                                                                                                                                                                                      acid chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                             l Similarity
18; Conserv
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                                                                                                                                                                                                                                                             AAP71135
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AGCAGGCCGCTGTCCTTG
                                                                        2712 BP;
                                                                                                                                                                                           Table 2; 16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAGGCCGCTGTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA; 2712
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llarity 100.0%;
Conservative
                             100.0%;
(larity 100.0%;
Conservative (
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(first entry)
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                                                                        519 A; 945 C; 849
                                                                                                                                                                                                                            glyco:protein
d for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                          type 1 (KOS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment; Herpes Simplex Virus-1;
          18
                             0
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Pred. No.
                                         Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 892
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                               Mismatches
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                                                                        <u>0</u>
                                                                                                                                                                                                                                      of HSV-1
                                                                                                                                                                                                                             herpes
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                                                                        397 T; 2
                                                   DB 8;
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                                                                                                                                                                                                                           and 2 - prepd. as
simplex virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                               <u>.</u>
                                                  Length 2712;
                                                                         other;
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                               Gaps
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RESULT 4
AAN71399/c
ID AAN71399 standard; DNA; 2724 BP.
XX
AC AAN71399;
XX
DT 25-MAR-2003 (updated)
DT 30-APR-1991 (first entry)
XX
DE Herpes Simplex Virus-2 gB from p521
XX
Vaccine; prophylaxis; treatment; He
XW 9lycoprotein; gB; ss.
XX
KW 9lycoprotein; gB; ss.
XX
PN US4642333-A.
XX
PN US4642333-A.
XX
PPN US4642333-A.
XX
PPN US4642333-A.
XX
PPN US4642333-A.
XX
PPN US4642333-A.
XX
PP 20-JUN-1984; B4US-0622496.
XX
PP 20-JUN-19
ARBSULT 5
AANSO517/c
ID AANSO5
XX AANSO5
XX AANSO5
XX 21-NOV
XX XX
DE Sequen
DE type 2
XX XX
XX Vaccin
XX Vaccin
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A pure non-glycosylated amino acid (AA) chain comprising a sequence corresponding to that occurring in glycoprotein B of HSV-1 or HSV-2 virus which is antigenic to HSV-1 of HSV-2, which contains no more than 750 AA residues, and which includes AA residues 135-649 inclusive is claimed. It can be used to produce vaccines for prophylaxis and treatment of HSV-1 and HSV-2. See AAN71303 for the HSV-1 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; prophylaxis; treatment; Herpes Simplex Virus-1; glycoprotein; gB; ss.
                                                                                  Sequence encoding the glycoprotein B (gB) of Herpes simplex virus type 2 (HSV-2).
                                                                                                                                                                                                                                                                                  AAN50517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2724 BP; 494 A; 911 C; 854 G; 390 T; 75 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid chain of glyco:protein B of HSV-1 and 2 - prepd. as recombinant and used for vaccines for herpes simplex virus types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes Simplex Virus-2 gB from p52BXX.
                          Vaccine; glycoprotein B;
                                                                                                                                                                       21-NOV-1991
                                                                                                                                                                                                                             AAN50517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'N' indicated nucleotide to be determined (corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                               2099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAGGCCGCTGTCCTTG
                                                                                                                                                                                                                                                                               standard; DNA; 2727
                                                                                                                                                                                                                                                                                                                                                                                                                               AGCAGGCCGCTGTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                       (first
                                                                                                                                                                     entry)
                             88
                                                                                                                                                                                                                                                                                                                                                                                                                               2082
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Pred. No. 34;
0; Mismatches
                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 6
AAV62146/c
ID AAV62146 standard; DNA; 2841 BI
XX
AC AAV62146;
XX
AC AAV62146;
XX
DT 07-DEC-1998 (first entry)
XX
HSV-2 strain SB5 Contig ID 91 I
XX
HSV-2 strain SB5; immunological
XW
Antiviral identification; viral
XX
OS Herpes simplex virus type 2.
XX
FH Key 1588..2745
FT CDS 358..2745
FT CDS /*tag= a
XX
XX
PN W09820016-A1.
XX
PD 14-MAY-1998.
XX
PF 31-OCT-1997; 97WO-US20016.
XX
PF 31-OCT-1997; 97US-0049018.
PR 09-JUN-1996; 96US-0030279.
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-SEP-1983;
23-JUN-1983;
20-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence corresponding to that occurring in glycoprotein B of HSV-or HSV-2. Preferably, when the chain comprises a sequence correspond to that occurring in glycoprotein B of HSV-2, it contains 4-750 M residues. The chain esp.has a molecular wt. of 65000 daltons and includes AA residues 165-629 from the HSV-2 glycoprotein B sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The inventors claim a non-glycosylated amino acid chain comprising a semience corresponding to that occurring in glycoprotein B of HSV-1
                                                                                                                                                                                                                           HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2727 BP; 493 A; 91,3 C; 855 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Table 2, Page 35-35C; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1985-039636/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Person
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PERS/) PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o acid chains of glyco-protein B of herpes simplex virus by recombination DNA methods for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAGGCCGCTGTCCTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                         SB5 Contig ID 91 DNA sequence.
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83US-0506986.
84US-0622496.
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                          Claim 6; Fig 8; 16pp; Japanese
                                                                                                                                     Polypeptide for herpes simplex virus vaccine prodn. - culturing transformant of recombinant DNA coding fuse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1989;
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and treatment of infection of
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glycoprotein. Such sequences have been used to develop synthetic DNA primers which have homologous sequences of conserved regions which flank a divergent region of the gB glycoprotein gene. In addition, proteins such as the gB glycoprotein have potential use in the development of serological immunoassays. One approach is to synthesize peptides which, based on the properties of the predicted protein sequence, are likely to be immunologically active. Such peptides can be used as substrate antigens in immunoassays to detect serum antibodies which recognize this specific peptide sequence. Synthetic peptides may also be used to produce antibodies against specific regions of the gB glycoprotein which are unique to one virus. These can then be used to develop virus specific primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The DNA sequence encodes a fusion protein comprising herpes simplex virus (HSV) surface antigens gB and gD. This fusion protein shows the same physiological activity as surface antigen prepd. from HSV infected cells. It can be used in a vaccine for the prevention of
                                                                                                                                                                                                                        Disclosure; Column 23-30; 22pp; English.
                                                                                                                                                                                                                                                   Detection of herpes B virus by PCR amplification of sample DNA -detect a specific herpes simian monkey B virus DNA segment.
                                                                                                                                                                                                                                                                                                                                            Black D,
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpes simian monkey SA8 virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SA8 virus gB glycoprotein coding sequence
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                                                                                                                                                                                            This sequence encodes the herpes simian monkey SA8 virus
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                                                                                                                                                                                                            The gene encodes a gB glycoprotein which is useful for the production of vaccines conferring protection against herpes simplex virus infections. The vaccine is Bafe in use and does not contain a carcinogenic gene, as with prior vaccines.

(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA containing herpes simplex virus gene or fragment useful in transformant yeast for prodn. of high purity herpes simplex virus glycoproteins for use in protective vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
31-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-herpes viruses and for identification of antibodies directed against SA8 virus in primate serum samples.
                                                                                                                                                                     Sequence 3098 BP;
                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig. 6; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1986-036935/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-1986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP170169-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSV; gb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAN60195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN60195 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2943 BP; 462 A; 1103 C; 983 G; 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nozaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KAGA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2140
2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 simplex virus glycoprotein gB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGCAGGCCGCTGTCCTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHEMO SERO THERAPEUTIC RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein; vaccine;
                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGGCCGCTGTCCTTG 2123
AGCAGGCCGCTGTCCTTG
                                      AGCAGGCCGCTGTCCTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Makizumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84JP-0151766.
84JP-0262465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85EP-0109042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
257..2966
                                                                                                                                                                     586 A; 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kino Y,
2335
                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                 Score 18; DB Pred. No. 34; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB
Pred. No. 34;
                                                                                                                                                                     ე
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eto,
                                                                                                                                                                     959 G; 483 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohtomo
                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T,
                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                   0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                          Length 3098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  z
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                               0;
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RESULT 11 AAQ14478/c

AAQ14478

standard;

DNA;

3465

ВP

0

AAQ14478; 25-MAR-2003 23-JAN-1992

(updated) (first entry)

HSVgB gene

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RESULT 10
AAN70681/c
ID AAN70681 standard; DNA;
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                       ફ
                                                                                             Matches
                                                          Query Match
Best Local
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10-MAR-2003
30-APR-1991
                                                                                                                                                  The gene encoding HSV gB is cloned into B.coli. To increase the efficiency of expression, the gene encoding the C-terminal region of gB, which is very hydrophobic, is removed and the remaining gene is cloned into an expression vector. The vector is composed of pBR322, SV40 early promoter and the HSV gB gene.

The construct is useful for the production of a good antigen for
                                                                                                                                                                                                                                                               Recombinant DNA contg. herpes simplex virus gene - is integrated in E.coli plasmid vector, contg. incorporated promoter region for animal cells, giving antigen.
                                                                                            Sequence 3461 BP; 666 A; 1188 C; 1041 G; 566 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN70681;
                                                                                                                                                                                                                                         Disclosure; Fig 3(1-3); 13pp; Japanese
                                                                                                                                                                                                                                                                                                                            WPI; 1987-183377/26.
                                                                                                                                                                                                                                                                                                                                                                          14-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                               JP62115288-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant
                                                                                                                   (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                P-PSDB; AAP70426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus; E.coli; plasmid; vector; promoter; antigen;
                                                                                                                                                                                                                                                                                                                                                  (KAGA ) KAGAKU OYOBI
                                                                                                                                            HSV vaccine.
2349
                        --
                                              l Similarity
18; Conserv
                        AGCAGGCCGCTGTCCTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein; HSV
AGCAGGCCGCTGTCCTTG 2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           herpes simplex virus gene
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(updated)
(first entry) '.
                                                                                                                                                                                                                                                                                                                                                                           85JP-0255971
                                                                                                                                                                                                                                                                                                                                                                                                  85JP-0255971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 254..2962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= HSV_gB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                    KESSEI RYOHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gB; ss.
                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          뫈
                                                          Score 18; DB
Pred. No. 34;
                                                Mismatches
                                                                      DB
                                                                     œ
                                               o
;
                                                                    Length 3461;
                                               Indels
                                              0
                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1989;
22-JUN-1989;
21-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence encodes the HSVgB polypeptide. The recombinant protein or esp. truncated forms of it, can be used to prepare vaccines for prophylaxis of HSV infection and for use in diagnostic kits. See also AAQ14479.
                        polyA_signal
                                                                                                  TATA_signal
                                                                                                                                              CAAT_signal
                                                                                                                                                                                                                             transmembrane anchor region; ss.
                                                                                                                                                                                                                                          Herpes simplex virus; HSV; type I; type II; glycoprotein B; vaccine; membrane protein; virus-specific glycoprotein;
                                                                                                                                                                                                                                                                                                                                                        AAT93650;
                                                                                                                                                                                                                                                                                                                                                                                   AAT93650 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3465 BP; 666 A; 1194 C; 1044 G; 561 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 1; 24pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSVgB polypeptide(s) obtd. by recombinant DNA techniques useful as vaccines against HSV and in diagnosis, can be p cheaply and safely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-328397/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP03218397-A.
                                                                                                                                                                                                                                                                                         Herpes simplex virus type 1 glycoprotein B encoding DNA
                                                                                                                                                                                                                                                                                                                         26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; antigen;
                                                                                                                                                                                                Негрев
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۳
                                                                                                                                                                                              simplex virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR14665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGGCCGCTGTCCTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGGCCGCTGTCCTTG 2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89JP-0308941.
89JP-0158238.
90JP-0161448.
                                           /*tage b
/note= "putative"
309..3023
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251..2965
                         /*Eag= C
                                                                                                                 /note= "putative"
         /*tage
                                                                                                                                                              Location/Qualifiers
                                                                                                                                    *tag= a
                                                                                                     25..131
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                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                     3471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
           PRINCE SERVING SERVING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 18
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06-APR-1984;
20-SEP-1990;
21-DEC-1992;
18-OCT-1993;
                                                                                                                  Herpes simplex virus.
                                                                                                                                                 Vaccine;
                                                                                                                                                                                                              25-MAR-2003
09-MAR-1992
                                                                                                                                                                                                                                                           AAN80907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW34552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-372022/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyA_signal
                           WO8802634-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5648079-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                      2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RL, Pachl C,
                                                                                                                                                                                                                                                                                                                                                                                                   ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             AGCAGGCCGCTGTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; llarity 100.0%; Conservative d;
                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86US-0921730.
84US-0597784.
90US-0587179.
92US-0993415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9308-0138717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0351875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...
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RESULT 13
AAN80907/c
ID AAN80907 standard; DNA; 3472 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is from the Herpes simplex virus (HSV) type I strain Patton and encodes a glycoprotein B. HSV is a double stranded virus packaged within an icosohedral nucleocapsid enveloped within a membrane. The membrane includes a number of virus-specific glycoproteins, with glycoprotein B being one of the most abundant. Glycoprotein B from both HSV type I and type II are cross reactive. New vaccines comprising recombinantly produced glycosylated glycoprotein B that has a deletion of at least part of the transmembrane anchor region, in combination with a carrier and an adjuvant have been produced. The vaccines are used for immunising humans against HSV (HSV type 1 or HSV type 2) by vaccination before or after primary infection with HSV.
                                                                                                                                                                                                               Sequence of Herpes simplex virus (HSV) glycoprotein B (gB) 1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3471 BP; 639 A; 1201 C; 1069 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4A-F; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccines against herpes simplex virus infection - containing recombinant HSV glycoprotein B
                                                                                                                                                     herpes simplex virus; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCAGGCCGCTGTCCTTG 2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "putative" 3409..3416
Location/Qualifiers 309..3023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Valenzuela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB
Pred. No. 34;
d; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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ARBSULT 14
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Best Local S
Matches 18
                                                                                                06-APR-1984;
20-OCT-1986;
20-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prepn. of recombinant gB and gD is described in W088504587. The amino acid sequence and DNA sequence for gB 1 presented in AAP80914 and AAN80907 differ from that originally presented in Table 1 of International Publication No. WO 85/04587. The DNA sequence in Table 1 contains an error in that an additional nucleotide (G) is listed at position 607 which resulted in a shift in reading frame relative to AAN80907 from which this nucleotide has been deleted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine for treatment of herpes simplex virus - recombinant HSV glyco:proteins B and D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; gB1; gB2; herpes simplex virus; HSV-1; HSV-2; flanking; initiation; termination; transcription; translation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3472 BP; 639 A; 1202 C; 1068 G; 563 T; 0 other;
                                                                                                                                                                                                                                                                                              US5244792-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Herpes simplex virus 1 strain Patton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ48496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 4; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1988-119368/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-1987;
20-OCT-1986;
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  Burke RL,
                                                                                                                                                                                             20-SEP-1990;
                                                                                                                                                                                                                                              14-SEP-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulatory sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ48496 standard; DNA; 3472 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-1988.
                                                (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĽR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP80914.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCAGGCCGCTGTCCTTG 2381
Pachl C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pachl C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
larity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
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                                                                                             84US-0597784.
86US-0921730.
90US-0587179.
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86US-0921213.
                                                                                                                                                                                             90US-0587179
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                                                                                                                                                                                                                                                                                                                                                                       309..3023
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
  Valenzuela PDT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valenzuela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 18; DB; Pred. No. 34; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۵,
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RESULT 15
AAQ48497/c
\texttt{C} \times \texttt{S} \times \texttt{P} + \texttt{P} \times \texttt{S} \times \texttt{P} \times 
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1984;
20-OCT-1986;
20-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA constructs for expressing a glycosylated polypeptide in a eukaryotic host cell comprises (1) an oligonucleotide sequence (08) free of natural flanking sequences, encoding glycoprotein B (gB) of HSV, or its fragments, and (2) 5' initiating and 3' terminating transcriptional and translational regulatory sequences flanking OS, at least one of these sequences not being from HSV. The HSV-1 and HSV-2 sequences are given in AAQ48496 and AAQ48497 respectively. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ48497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein
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                                                                                                   Disclosure;
                                                                                                                                                                                            DNA construct for expressing HSV glycosylated polypeptide useful for vaccinating against HSV-1 and -2 infections
                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR41779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burke RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5244792-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus 2 strain 333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory sequence; ss.
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29-MAR-1994
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P-PSDB; AAR41778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2398 AGCAGGCCGCTGTCCTTG 2381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pachl C,
                                                                                        Fig 4; 33pp; English.
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(first entry)
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86US-0921730.
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/*tag= a
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Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDT;
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DNA constructs for expressing a glycosylated polypeptide in

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
        of hits satisfying chosen parameters:
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Compugen
                                Sequence 13, Appl
Sequence 13, Appl
Sequence 7, Appli
Sequence 7, Appli
Patent No. 5244792
Patent No. 5244792
Patent No. 5244792
Sequence 1201, Appli
Sequence 15, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 12195, A
Sequence 12195, A
Sequence 12195, A
Sequence 12303, A
Sequence 12303, A
Sequence 12301, A
Sequence 24, Appl
Sequence 24, Appl
Sequence 11, Appl
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US-08-804-439A-13/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYCOPPOTEIN B
TITLE OF INVENTION: SUBFAMILY OF HE
NUMBER OF SEQUENCES: 113
                                                   Query Match
Best Local S
Matches 18
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                                                                                                                         INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDEDMESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                  ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,439A
FILING DATE: Pebruary 21, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 39,347
REFERENCE/DOCKET NUMBER: 09176/004001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Fish & Richardson P.C.
STERET: 4225 Executive Square, Ste
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                            TELEFAX: (619) 678-5099
TELEX:
2096
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o. 6015565
                                                     l Similarity
18; Conserv
                AGCAGGCCGCTGTCCTTG
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                                                   100.0%; Score 18; DB:
ilarity 100.0%; Pred. No. 6.4;
Conservative 0; Mismatches
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US-08-851-089-12
US-08-851-089-13
US-08-851-089-13
US-08-476-519-10
US-08-476-519-10
US-08-476-519-1
US-08-629-939-1
US-08-629-939-1
US-09-103-840A-2
US-09-103-840A-1
US-09-103-840A-1
US-09-252-991A-263
US-09-252-991A-15658
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HERPES VIRUSES
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                                                                                Length 2713;
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Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1244, Ap
Sequence 2, Appli
Sequence 1, Appli
Sequence 6122, Appli
Sequence 6122, Appli
Sequence 6122, Appli
Sequence 6122, Appli
Sequence 12658, Ap
Sequence 11658, A
Sequence 246, App
Sequence 21658, A
Sequence 21658, A
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US-08-720-229-13/c
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTION DATA:
APPLICATION UMBER: US/08/720,229
FILING DATE: 26-SEP-196
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION UMBER: 40,253
REFERENCE/DOCKET NUMBER: 29938-20002.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-0792
TELEPAN: (415) 494-0792
                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08042747A Patent No. 5487969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 18; Conservative
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Best Local |
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                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Eberle, Richard
APPLICANT: Black, Darla
APPLICANT: Scinicariello, Franco
APPLICANT: Scinicariello, Franco
APPLICANT: Hillard, Julia K.
TITLE OF INVENTION: Cloning and Amplification of Monkey B
TITLE OF INVENTION: Virus Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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TELEX: 706141
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROBE, Timothy M.
APPLICANT: BOSCH, Marnix L.
APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
NUMBER OF SEQUENCES: 100
CORRESSENCE ADDRESS:
                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: dou
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STATE: CA
COUNTRY: USA
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                    COUNTRY:
                                  CITY: San Antonio
STATE: Texas
                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304-1018
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                                                                                              ADDRESSEE:
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Similarity 100.0%; Pred. No. 6.4
18; Conservative 0; Mismatches
78205
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                                                                         E: Cox & Smith Incorporated 112 East Pecan Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Morrison & Foerster
755 Page Mill Road
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B FROM HERPES SIMPLEX VIRUS

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION NUMBER: US/08/58

APPLICATION NUMBER: US/08/58

PILING DATE: 20-SEP-1990

PRIOR APPLICATION NUMBER: 921,730

FILING DATE: 20-OCT-1986

APPLICATION NUMBER: 597,784
RESULT 5
5244792-2/c
;PATENT NO. 5244792
; PATENT NO. 5244792
; APPLICANT: BURKE, RAE L.;PACHL, CAROL;VALENZUELA, PABLO D.
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT GLYOPROTEIN
;B FROM HERPES SIMPLEX VIRUS
; NUMBER OF SEQUENCES: 19
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5244792-1/c
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                                                                                                                                                                                                                                                                                                                                                             5244792-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Patent No. 5244792
; APPLICANT: BURKE, RAE L.;PACHL, CAROL;VALENZUELA, PABLO D.T.;
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT GLYOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 6.4; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
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INFORMATION FOR SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNBY AGENT INFORMATION:
NAME: Haymond, W. Bradley
REGISTRATION NUMBER: 35186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/042,747A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 210-554-5500
TELEPHX: 210-226-8395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-APR-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 87..2744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acta STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2943 base pairs
                                                                                                                                                                                                  2398
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                                                                                                                                                                                                    AGCAGGCCGCTGTCCTTG 2381
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1201
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                                         NUMBER OF SEQ ID NOS:
SEQ ID NO 1243
LENGTH: 1491
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1998-07-:
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1201
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Sequence 1243, Application US/09252991A Patent No. 6551795
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                    APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ABBUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
-09-252-991A-1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/58
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 921,730
FILING DATE: 20-OCT-1986
                 TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 855
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17; Conserv
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Pred. No. 6.4;
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US-08-076-726-15/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1362
LENGTH: 1551
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,726
FILING DATE: 14-UN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.2490001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/08076726 Patent No. 5464758
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                                                                                                                                                                                                                                                     STREET: 1100 New York Avenue, N.T.
CITY: Washington
STATE: District of Columbia
COUNTRY: United States of America
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TITILE OF INVENTION: EUNOMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gossen, Manfred APPLICANT: Bujard, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 94.4%; Score 17; DB Local Similarity 100.0%; Pred. No. 19;
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(202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US 60/074,788
1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tight Control of Gene Expression in Eucaryotic Cells by Tetracycline-responsive Promoters
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                                                                       US-08-260-452-8
Query Match
Best Local S
Matches 17
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076,327
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6244 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 17; Conserv
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APPLICANT: Gossen, Manfred
APPLICANT: Bujard, Hermann
APPLICANT: Salfeld, Jochen
APPLICANT: Salfeld, Jochen
APPLICANT: Voss, Jeffrey
TITLE OF INVENTION: Tight Control of Gene Expression in Eucaryotic
TITLE OF INVENTION: Cells by Tetracycline-responsive Promoters
NUMBER OF SEQUENCES: 10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6244 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
                                                                                                                                         ORGANISM:
                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
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1 Similarity
17; Conserv
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                                                                                                                      Towne (hCMV)
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94.4%; Score 17; DB 1; ilarity 100.0%; Pred. No. 19; Conservative 0; Mismatches
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                                                                                                                                         Human cytomegalovirus
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                                                                                                                                                                                              circular
                                                                                                                                                                           DNA (genomic)
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/ 100.0%; Prr
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19;
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                                Length 6244
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RESULT 11
US-08-481-970-8/c
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GENERAL INFON----
APPLICANT: GOSSEN, Man---
APPLICANT: Salield, Jochen
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Teffrey
                                                                                                      Query Match
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                                                                      Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,970
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/260,452
PILING DATE: 14-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/76,327
PILING DATE: 14-JUN-1993
ATTORNEY/AGENT IMFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 227-59
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                       ORGANISM: Human cytomegalovirus STRAIN: Towne (hCMV)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Voss, Jeffrey
TITLE OF INVENTION: Animal Transgenic for a Tetracycline-Controlled
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 6244 base pairs
                                                                    Local Similarity 100.0%;
les 17; Conservative (
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                                      1 AGCAGGCCGCTGTCCTT 17
                                                                                                                                                                                                                                                                                           nucleic acid
AGCAGGCCGCTGTCCTT 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                             circular
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                                                                                                                                                                                                                                                                                                                                                                                   (617)
                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                               double
                                                                                                                                                                                                                                                                                                                                                                227-5941
                                                                                                                                                                                                                                                                                                                                                                                 227-7400
                                                                                        94.4%; Score 17; DB
100.0%; Pred. No. 19;
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                                                                        Mismatches
                                                                                                       DB 2; Length 6244;
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RESULT 12 US-08-897-719-8/C ; Sequence 8, Application US/08897719 ; Patent No. 5922927

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US-09-163-269-8/c
                                                                                                                                                    Patent No. 6252136
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6244 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                        Matches
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MOLECULE TYPE: D
ORIGINAL SOURCE:
           APPLICANT: Gossen, Manfred
APPLICANT: Bujard, Hermann
APPLICANT: Salfeld, Jochen
APPLICANT: Voss, Jeffrey
TITLE OF INVENTION: Animal Transgenic for a Tetracycline-Controlled
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEB: Lahive & Cockfield
ADDRESSEB: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human cyto
STRAIN: Towne (hCMV)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 14-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-013CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Tight Control of Gene Expression in Eucaryotic TITLE OF INVENTION: Cells by Tetracycline-responsive Promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                               991 AGCAGGCCGCTGTCCTT 975
                                                                                                                                                                                                                                                                                                                                                                      l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02109-1875
                                                                                                                                                                                                    Application US/09163269
                                                                                                                                                                                                                                                                                                                                  AGCAGGCCGCTGTCCTT 17
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60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Voss, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gossen, Manfred
Bujard, Hermann
Salfeld, Jochen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                    94.4%; Score 17; DB 2;
100.0%; Pred. No. 19;
tive 0; Mismatches
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                                                                     Transcript:
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TITLE OF INVENTION: NUCLBIC ACID AND AMINO A TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTI FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-07-27
NUMBER OF SEQ 1D NOS: 33142
SEQ ID NO 12195
LENGTH: 711
                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12195
                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-252-991A-12195/c
                                                                                                                                                                                                                                                                                             Sequence 12195, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZITE: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,269
                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 6244 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: 14-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: GILLIO A. DECONCI, Jr
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                           ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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NUCLBIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Query Match Best Local Similarity

91.1**%**; 94.4**%**;

Score 16.4; Pred. No. 36;

DΒ 4.

Length 711;

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Darzine, Aldis
APPLICANT: Xi, Lei
APPLICANT: Xi, Lei
APPLICANT: Childs, John D.
APPLICANT: Monticello, Daniel J.
APPLICANT: Monticello, Daniel J.
APPLICANT: MONTICE SUITES H.
TITLE OF INVENTION: DSZ Gene Expression In Pseudomonas Hosts
NUMBER OF SEQUINCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
ZIP: 02173
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Search completed: September 16, 2003, 20:42:36 Job time: 27.9901 secs
                                                                                                                                                                                                                                                  US-08-851-088-9
                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/835,185
PILLING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elmore, Carolyn S.
REGISTRATION NUMBER: 37,567
REFERENCE/DOCKET NUMBER: EBC96-06A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (781) 861-6240
TELECHONE: (781) 861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 Dase pairs
                                                                                                                                                            Query Match
Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,088
PILING DATE: 05-MAY-1997
                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1107
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                               620 AGCAGGCCGCAGTCCTTG 637
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Maximum DB
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08 NEW PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US108 PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US108 PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US108 PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US108 PUBCOMB.seq:*

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17: /cgn2_6/ptodata/2/pubpna/US108 PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US108 PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US108 PUBCOMB.seq:*
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Match Length
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18
    Maximum Match 100%
Listing first 45 s
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                1431
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    13 US-10-027-632-12963

US-10-027-632-22964

9 US-09-832-312-24

10 US-09-832-312-11

12 US-10-143-618-19

14 US-10-139-662-19

14 US-10-139-683-19

14 US-10-139-683-19

14 US-10-139-683-19

14 US-10-139-683-19

15 US-10-198-846-11382

16 US-9-764-868-222
                                                                                                                                                                                     US-09-815-242-7812
US-09-281-674-8
US-09-892-227-8
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Sequence 8, Appli
Sequence 7812, Ap
Sequence 8, Appli
Sequence 8, Appli
Sequence 1293, A
Sequence 1294, A
Sequence 24, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 1332, Ap
Sequence 222, App
Sequence 222, App
Sequence 21382, Ap
Sequence 21382, Ap
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | S S | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 |
| 14.8 | | ٠ | 14.8 | 14.8 | | 14.8 | 14.8 | | 14.8 | 14.8 | 14.8 | 15 | 15 | 15 | 15 | 15 | 15.4 | 15.4 | 15.4. | 15.4 | 15.4 | 15.4 | 15.4 | 15.4 | 15.4 | 15.4 | 15.4 | 15.4 |
| 82.2 | 82.2 | | | 82.2 | 82.2 | 82.2 | 82.2 | 82.2 | 82.2 | 82.2 | 82.2 | 83.3 | 83.3 | | | | | 85.6 | 85.6 | 85.6 | 85.6 | 85.6 | 85.6 | 85.6 | 85.6 | 85.6 | 85.6 | 85.6 |
| 810 | 765 | 618 | 478 | 471 | 439 | 439 | 424 | 371 | 371 | 262 | 60 | 3446 | 1929 | 1332 | 263 | 262 | 9025608 | 23098 | 5003 | 2799 | 2519 | 2470 | 2470 | 2470 | 2470 | 2453 | 2190 | 622 |
| 14 | 11 | 12 | 13 | H | 14 | 5 | IJ | 14 | 10 | 9 | 12 | 12 | 14 | 9 | 9 | 9 | 1 | | <u>14</u> | 9 | ü | 12 | 10 | 10 | 9 | 10 | 14 | 13 |
| US-10-156-761-2123 | US-09-975-719-324 | US-10-308-279-67 | US-10-027-632-287388 | US-09-918-995-32269 | US-10-040-862-2556 | US-09-796-692-2556 | US-10-001-857-58 | US-10-040-862-6249 | US-09-796-692-6249 | US-09-923-876-2088 | US-09-908-975-13289 | US-09-769-734-4 | US-10-106-698-805 | US-09-250-883-14 | US-09-250-883-2 | US-09-250-883-1 | US-10-156-761-1 | . US-10-017-161-2005 | US-10-207-655-62 | US-09-935-368-2 | US-10-071-766-82 | US-10-354-358-7 | US-09-880-107-1725 | US-09-954-456-1121 | US-09-870-937-9 | US-09-974-298-111 | US-10-156-761-2735 | US-10-027-632-267576 |
| 2123, | 324 | Sequence 67, Appl | æ | | 2556, | 255 | Sequence 58, Appl | 624 | е 6249, | | 13 | | e e | | Ν | • | Œ | Sequence 2005, Ap | Sequence 62, Appl | ٧, | 82 | 7 | 17 | Sequence 1121, Ap | 9, Apı | 111, / | Sequence 2735, Ap | Sequence 267576, |

ALIGNMENTS

US-09-827-688-8

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RESULT 2
US-09-815-242-7812/c
                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                    US-09-827-688-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09827688
Publication No. US20030165476A1

GENERAL INFORMATION:
APPLICANT: ORSON, FRANK
APPLICANT: KINSEY, BERMA
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION D
TITLE OF INVENTION: AGENTS
FILE REFERENCE: P01949US1/1004014
CUGRENT APPLICATION NUMBER: US/09/827,688
CUGRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR FILING DATE: 2000-04-07.
NUMBER OF SEQ ID NOS: 13
Sequence 7812, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                   Best Local Similarity 100.0%; Score 18; DB Matches 18; Conservative n. Minner
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: HERPESVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 154746
                                                                                                                                                                                          DB 12;
                                                                                                                                                                                                                                                                                                                        Length 154746;
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; LOCATION: (1)...(1431)
US-09-815-242-7812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
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FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION UNMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conserv
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Patent No. US20020077307A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7812
LENGTH: 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                  ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/281,674
FILING DATE: 30-MAY-1999
CLASSIFICATION: UNKnown>
                                                                                                                                                                                                                                                                                                                                                    VOSS, Jeffrey
TITLE OF INVENTION: Methods for Regulating Gene Expression
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gossen, Manfred
Bujard, Hermann
Salfeld, Jochen
  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 GCAGGCCGCTGTCCTTG 348
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                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lahive & Cockfield STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind, Judith W. Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto, Robert T.
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100.0%; Pr
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20;
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; IMMEDIATE SOURCE:
; CLONE: DUHD BGR3
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-281-674-8
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US-09-892-227-8/c
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Patent No. US20020152487A1
GENERAL INFORMATION:
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                                  COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,227
FILING DATE: 25-Jun-2001
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/163,269
FILING DATE: 4Unknown>
APPLICATION UNMBER: 09/163,269
FILING DATE: 14-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/479,306
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: 08/260,452
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: 08/076,327
FILING DATE: 14-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: GAULIO A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-013CP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                               ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Animal Transgenic for a Tetracycline-Controlled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gossen, Manfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human cytomegalovirus
NAME: Giulio A. DeConti, Jr. REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)
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Salfeld,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.4%; Score 17; DB 9; 100.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hermann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jochen
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Length 6244;

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RESULT 6
US-10-027-632-12964
; Sequence 12964, Application US/10027632
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-027-632-12963
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                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                    SEQ ID NO 12963
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Best Local
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
PRIOR
PRIOR
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                       TYPE; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/156,358 FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-03-29
APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: DUHD BGR3
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human cytomegalovirus STRAIN: Towne (hCMV)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                    DNA
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                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6244 base pairs
TYPE: nucleic acid
TYPE: double
                                                                                                     AGCAGGCCCCTGTCCTTG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                     Conservative
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                                                                                                                                                                                    91.1%;
94.4%;
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                                                                                                                                                                                    Score 16.4;
Pred. No. 4!
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Pred. No.
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                                                                                                                                                                                                   DB 13;
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                                                                                                                                                                                                   Length 609;
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; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Homo s
US-09-832-312-24
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                                                     Query Match
Best Local Similarity
Workshes 17; Conserve
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US-09-832-312-24/c
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR PELICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR PELION OFFE: 2000-04-20

PRIOR PELION OFFE: 2000-04-20

PRIOR PELION OFFE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR PILING DATE: 1999-11-23

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                      SOFTWARE: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 325720
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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CURRENT FILLING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 78
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 7853-234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 609
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les 17; Conserv
1496
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                                                                                                                                                                                                                                                       FastSEQ for Windows Version
AGCAGGCCCCTGTCCTTG 1479
                                AGCAGGCCGCTGTCCTTG 18
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                                                                            Conservative
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94.4%;
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94.4%;
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                                                                                          Score 16.4;
Pred. No. 39
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Pred. No. 45;
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                                                                                                               Length 1896;
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; TYPE: DNA
; ORGANISM: Homo mapiens
US-09-832-312-11
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; ORGANISM: Homo sapiens
US-09-954-456-960
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                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR APPLICATION NUMBER: 09/345,468
                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09832312 Patent No. US20010049829A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-832-312-11/c
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES
FILE REFERENCE: 7853-234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEO ID NOS: 2276
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                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
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PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
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                                                                                                                                                   PRIOR FILING DATE: 1999-06-30
                                                             LENGTH: 2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/60/235,840 FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/60/235,134 FILING DATE: 2000-09-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/60/235,638 FILING DATE: 2000-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/60/235,637
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Pred. No. 39
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RESULT 10
US-10-143-618-19/c
US-10-143-618-19/c
; Sequence 19, Application US/10143618
; Publication No. US20030166073A1
; Publication No. US20030166073A1
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APPLICANT: Cosman,
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                           Match 91.1%; Score 16.4; Local Similarity 94.4%; Pred. No. 38
                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 67..1959
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/143,618
FILING DATE: 08-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1545
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1562 AGCAGGCCCCTGTCCTTG 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                       1 AGCAGGCCGCTGTCCTTG 18
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OPERATING SYSTEM: Microsoft Word 7.0
SOPTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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Pred. No. 38
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Immunoglobulin-Like Receptors
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RESULT 11 US-10-139-662-19/c J Sequence 19, Application US/10139662 Publication No. US20030027358A1

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RESULT 13
US-09-764-891-7432/c
; Sequence 7432, Application US/09764891
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US-10-139-683-19/c
; Sequence 19, Application US/10139683
; Publication No. US20030060614A1
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Best Local :
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                                                                                                                                                                              Matches
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TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
TITLE OF INVENTION: Like Receptors (LIR)
FILE REFERENCE: 2624-A
CURRENT APPLICATION NUMBER: US/10/139,662
CURRENT FILING DATE: 2002-05-02
FRIOR APPLICATION NUMBER: 09/310,463
FRIOR APPLICATION NUMBER: 09/310,463
FRIOR FILING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: 08/842,248
FRIOR APPLICATION NUMBER: 08/842,248
RIOR APPLICATION NUMBER: 08/842,248
RIOR APPLICATION NUMBER: 09/310,463
FRIOR APPLICATION NUMBER: 08/842,248
RIOR APPLICATION SUMBER: 08/842,248
RIOR FILING DATE: 1997-04-24
NUMBER: 0F SEQ ID NOS: 39
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CURRENT APPLICATION NUMBER: US/10/139,683
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/310,463
PRIOR FILING DATE: 1999-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cosman, David J.
APPLICANT: Anderson, Dirk M.
APPLICANT: Borges, Luis
TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
TITLE OF INVENTION: Like Receptors (LIR)
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                           FRATURE:
NAME/KEY: CDS
LOCATION: (67)..(1962)
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NAME/KEY: CDS
LOCATION: (67)..(1962)
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RESULT 15
US-09-764-868-222
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; ORGANISM: Homo sapiens
US-09-764-891-7432
                                                                     Sequence 222, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT332
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11382
Prior application data removed - refer to PALM NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 222
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SEQ ID NO 7432
LENCTH: 13553
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzher
APPLICANT: Steinmann, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: THERAPY OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 489

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (424)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (441)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (441)

OTHER INFORMATION: n equals a,t,g, or c

US-09-764-866-222

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 10; Length 489;

Best Local Similarity 94.1%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AGCAGGCCGCTGTCCTT 17

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Search completed: September 16, 2003, 22:54:15

Job time: 71.0495 secs
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| | | | 10 | 14 | 13 | 29 | 10 | 14 | 10 | 28 | 13 | 28 | 29 | 14 | 28 | 14 | 28 | 28 | 11 | 29 | 29 | 29 | 13 | <u>٦</u> | 띦 | 10 | 9 | 28 | ⊷ | 13 | 28 | 10 | 10 | 13 | 13 | 9 | 13 | 13 | 13 | |
| _ | 6522 | 0423 | BE540693 | D4580 | U25525 | 8353 | BG367557 | CA504539 | m | Η | -1 | BH328864 | 22 | | ű | • | m | • | 281 | 656 | BZ571854 | BZ578934 | 367 | BU937820 | BU134166 | BE410139 | AI296995 | AZ321116 | \vdash | 4073 | 8886 | w | E49043 | Q31701 | Y2232 | 66144 | T09901 | Y66155 | Y064 | BY664919 |
| AŪ09891 | 5227 psM | 4235 IL5-CI0 | 3 6010 | 58065 Fg08_04d | 55259 60374 | 83539 CH230 | 7 HVSME | 9 UI-R- | 2 EST45 | 77926 | NISC | 4 CH23 | CH230-25 | 3 AMG | v | 9 AMGNNI | 7 CH230- | 6 1008049H | C028153 Homo s | 556562 pacel-60 | 71854 msh2 2 | 8934 msh2 607 | 53678 |) AGENCOUR | U١ | 410139 60130245 | AI296995 LP11136.5 | O١ | 53914 MMSP0049 | 240732 TaE05013 | 88864 RPCI-11- | G633702 AT29407. | 90435 WHE0367 | 17016 IL3-CT02 | 223280 BY223 | 61443 AV66144 | Y066019 BY06601 | Y661558 BY6615 | 064920 BY06492 | 9 BY66491 |

ALIGNMENTS

RESULT 1 AW663294/c LOCUS DEFINITION JOURNAL COMMENT REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM Unpublished
Other ESTs: hh77al0.xl
Other ESTs: hh77al0.xl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Emmert-Buck, M.D., Ph.D. CDNA Library Arrayed by: Christa Prange, The
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
Technologies, Inc. CDNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be Bukaryota; Metazoa; Chordata; Craniata; Verte Mammalia; Butheria; Primates; Catarrhini; Hom 1 (bases 1 to 195)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute, Cancer Genome Anat Tumor Gene Index AW663294 195 bp mRNA linear EST 06-APR-2000 hh77a10.y1 NCI CGAP GUI HOMO SADIENS CDNA CLONE IMAGE:2968794 5' similar to TR:Ō15471 O15471 MONOCYTE INHIBITORY RECEPTOR PRECURSOR.: mRNA sequence. EST AW663294 AW663294.1 Homo sapiens Homo sapiens (human) GI:7455836 Craniata; Vertebrata; l Catarrhini; Hominidae; Anatomy Project (CGAP), Euteleostomi; Homo.

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          763918
TG3918
TG3918
TC08C12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE.80086 5' similar to SP.RET2_RAT P06768 RETINOL-BINDING
PROTEIN II, CELLULAR ;, mRNA sequence.
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                                                                                                                                                                 High gality sequence stops: 271 Source: IMAGE Consortium, LLML clone is available royalty-free through LLML; contact the IMAG Consortium (info@image.llnl.gov) for further information. Insert Length: 779 Std Error: 0.00
                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
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                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Insert Size: 779
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                     quality sequence stop: 271.
Location/Qualifiers
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2968794"
/tissue_type="2 pooled high-grade transitional cell
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:483703"
/db_xref="taxon:9606"
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Pred. No. 2.3e+03;
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FOCUS
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AZ081267
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Murphy, W. J., Sun, S., Chen, Z.-Q., Yuhki, N., Hirschmann, D., Menotti-Raymond, M. and O'Brien, S.J.

A radiation hybrid map of the cat genome: implications for comparative mapping Genome. Res. 10 (5), 691-702 (2000)
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                                                                                                                                                                                                                                            Similarity
17; Conserv
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Laboratory of Genomic Diversity
National Cancer Institute-FCRDC
P.O. Box B, Bldg. 560, Rm.11-10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Felis catus (cat)
Felis catus
BY310214
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Fax: 301 846 6327
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Mammalia; Butheria; Carnivora; Fissipedia; Felidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murphywi@mail.ncifcrf.gov
PCR with specific primers
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
/clone_lib="Felis catus
71 c 75 g 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Felis catus"
/mol_type="genomic DNA"
/strain="Fca215"
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Pred. No. 2.6e+03
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Pred. No. 2.5e+03;
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BY310214 RIKEN full-length enriched, stroma cell Mus musculus cDNP

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                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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prepare mouse tissues.
Tissues were provided by Takashi Ishikawa ( Department of Surgery
                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                  Nikaido, I., Osato, N., Satto, R., Suzuki, H., Yamanaka, I., Kyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., LE, Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gastberland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedziarski, R.M., Gough, J., Grimmond, S., Rurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Reid, J., Ring, R., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Xanasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, R.D., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Yang, L., Yuan, Z., Zavolan, M., Zih, Y., Zimmer, A., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zih, Y., Zimmer, A., Arakawa, T., Fukuda, S., Hashizme, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, S., Rosers, J., Birney, E. and Hayashizaki, Y.
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Laboratory for Genome Exploration Research Group, Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 364)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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                                                         Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/cell type="RIKEN full-length enriched, stroma cell"
/clone_lib="RIKEN full-length enriched, stroma cell"
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="1320013G01"
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94.4%;
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Institute of Physical and Chemical Research (RIKEN)

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BASE CO
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ORGANISM
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BY064920
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa, Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schombach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGCAGGCCGCTGTCCTTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:hhttp://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozar,T., Inotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,J., Inotani,K., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,J., Murata,M., Nakamura,M., Nomura,K., Shibata,K., Shiraki,T., Tagami,M., Maki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                             (bases 1 to 366)
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                                                                                                                                                                                                                                                                                                                                          366 bp mRNA linear EST 06 RIKEN full-length enriched, 17 days embryo heart cDNA clone 1920038D20 5', mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:10090"
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/dev_stage="14.5 days embryo RP+/+"
/clone_lib="RIKEN full-length enriched, 14.5 days embryo
RP+/+_Rathke's pouches"
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Pred. No. 2.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
MRL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    visit our web site (http://genome.gsc.riken.go.jp)
                                                                                        /clone_lib="RIKEN full-length heart"
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                          /tissue_type="heart"
/dev_stage="17 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Nibata,K., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shizaki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Computational Analysis of Full-Length Mouse cDNAs Compared with fuman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
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Nikaido, I., Osato, N., Salto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, R.J., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Waltanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes. Genome Res. 10 (10), 1117-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 388)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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Tissues were provided by Michelle Brinkmeier and Sally Camper (
Dept. Human Genetics University of Michigan Medical School 4301
MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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RIKEN full-length enriched, 17 days embr
cDNA clone I920046H19 5', mRNA sequence.
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/dev stage="14.5 days embryo RP+/+"
/clone_lib="RIKEN full-length enriched, 14.5
/RP+/+ Rathke's pouches"
79 c 79 g 105 t'
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="K720011A10"
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94.4%;
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d, 17 days embryo heart Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-Length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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The Institute Oppsical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@ggc.riken.go.jp,
URL:http://genome.ggc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazuma,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
,Sakazuma,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
,Sakazuma,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,Y. Direct
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Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="17 days embryo"
/clone_lib="RIKEN full-length enriched, 17 days embryoheart"
                              GLC Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mo_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="1920046H19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _type="mRNA
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                                                                                                                                                                                                                                                                                                                            Score 16.4; DB 13
Pred. No. 2.7e+03;
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                                                       391 bp
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GLCGSE03 3',
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AUTHORS
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AUTHORS
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, L.E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Godzik, A., Frazer, K.S., Gassterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons
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Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li.N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                 Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 424)

Language T Adachi.J. Bono, H., Kondo, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human
351 Guo Shoujing Road,
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY223280 RIKEN full-length enriched, activated cDNA clone F830302M06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV661443.1
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Tel: 86-21-50801919(ex.45)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l: hanzg@chgc.sh.cn
clone is available at CHGC in Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="mRNA"
/db xrefa"taxon:9606"
/clone="GLCGSE03"
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Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
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Pred. No. 2.7e+03;
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COMMENT
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                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.in) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Saeaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
Sakazume,N., Saeaki,D., Sato,K., Shiraki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues
Tissues were provided
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA
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            Conservative
                                                                                                                                                                                                         90
                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="8830302M06"
/tissue_type="activated spleen"
/clone_Tib="RIKEN full-length enriched, activated spleen"
/clone_Tib="RIKEN full-length enriched, activated spleen"
                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="NOD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                        91.1%;
94.4%;
        0
                                            Score 16.4;
Pred. No. 2.
                                            .8e+03;
                                                                                DB 13;
                                                                                Length 424;
        Indels
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RESULT 12
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LOCUS
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                                            DEFINITION
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ACCESSION
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                                                                                                                                                                                       89
              BE490435 522 bp mRNA linear EST 31-JUL-2000 WHE0367_D11_G21ZS Wheat cold-stressed seedling cDNA library Triticum aestivum cDNA clone WHE0367_D11_G21, mRNA sequence.
                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 442)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
BE490435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL3-CT0214-150200-076-F11 CT0214 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL3&t2=IL3-CT0214-
150200-076-F11&t3=2000-02-15&t4=1)
                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                 AGCAGGCCGCTGTCCTTG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="CT0214"
/note="Organ: colon; Vector: pucl8; Site_1: SmaI; Site_2:
/note="Organ: colon; Vector: pucl8; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
                                                                                                                                                                                                                                                                                                                                                                                                mRNA and cDNA amplification were performed under low
stringency conditions."
1 114 c 120 g 104 t
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|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                     91.1%;
                                                                                                                                                                                                                                                                                                     Score 16.4; DB 13;
Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                               Mismatches
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                   296
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metaza, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                        BG633702 546 bp mRNA linear EST 23-APR-: AT29407.5prime AT Drosophila melanogaster adult testes pOTB7 Drosophila melanogaster cDNA clone AT29407 5 similar to CG8214: FBan0008214 located on: 2R 52C2-52C2;: 04/09/2001, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 seq primer: Strategene SK primer.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i (bases 1 to 522)
Anderson.O.D., Chao, S., Choi, D.W., Close, T.J., Fento, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rau Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion genomes - Cold-stressed seedling cDNA library
                                                                                                     BG633702
BG633702.1 GI:13761239
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Olin Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /CLBBUELTYPE SUCULARY
/dev Energe="Five-day old seedling"
/lab_host="E. coli SOLR"
/clone_lib="Wheat cold-stressed seedling cDNA library"
/clone_lib="Wheat cold-stressed seedling cDNA library"
/clone_lib="Wheat cold-stressed seedling cDNA library"
/clone_lib="Wheat cold-stressed seedling cpnagemid;
site_l: Ecori Site_2: Xhoi; Seeds were surface-sterilized
Site_l: Ecori Site_2: Xhoi; Seeds were surface-sterilized
seedlinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Five-day
old seedlings were transferred to 5 Coold room and kept
for 48 hr. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
were in vivo excised to give pBluescript phagemids in the
TU Close lab (Choi, Close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
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/clone="WHE0367_D11_G21"
/tissue_type="Seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Chinese Spring'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Triticum aestivum"
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                                                                                                                                                                           mRNA sequence.
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                 Unpublished
Other GSS8: RPCI-11-266G3.TJ
Contact: Shaying Zhao, William Nierman,
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD :
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 554) Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
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Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ488864
RPCI-11-266G3.TV RPCI-11
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Location/Qualifiers
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                                                                                                                                                             Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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GSS.
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/lab host="plates AT.10-AT.120; DH5-alpha. Plates
AT.112-AT.319; DH5-alpha TonA"
/Clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/note="forgan: ADULT testes; Vector: pOTB7; Site_1: EcoRI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated CDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
a 138 c 153 g 99 t
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|mol type="mRNA"
|db xref="teaxon.7227"
|clone="AT29407"
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94.4%;
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Pred. No. 2.9e+03;
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                                                                                                                                                                                                                                        Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 013 row: E column: 12
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
BQ240732
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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17; Conserv
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TaE05013E12R TaE05 Triticum aestivum cDNA clone TaE05013E12R, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wheat functional genomics - Glenlea developing seeds cDNA libraries
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/db_xref="GDB:7601906"
/db_xref="taxon:9606"
/clone="RPCI-11-266G3"
/sex="Male"
/cell type="Lymphocytes"
/clone jlb="RPCI-11"
/note="Vector: pBACe3.6; Site 1: Ec
RPCI11 Human Male BAC Library"
3 a 148 c 84 g 159 t
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/tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host=#E. coli DH10B"
/clone_lib="TaE05"
                                                                                                                                  /organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Glenlea"
                                                                                          /db_xref="taxon:4565"
/clone="TaE05013E12R"
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                   /notes"Vector: pSPORT-P (Invitrogen Technologies); Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 5 days post-anthesis" a 121 c 157 g 150 t
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                              Query Match 91.1
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AGCAGGCCGCTGTCCTTG. 18
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Search completed: September 16, 2003, 20:39:53 Job time: 915.049 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| | WEITEDOOD LIBRE BOL | | Hernen | Human h | M21629 Herpes simp | M14164 HSV1 (strai | COGIN | Ž | 5 | Š | SH | DNA | NA encodin | 1 HSV-1 (E | Sequence | | | Sequence | 794 Vaccine | 92 Va | | DNA | DNA | DNA sequenc | 3 HSV2 glyc | | DNA enc | 5 Human | Human | Human | uman herp | Human he | | uman herp | 0 Human he | 28 Human he | 23 Human h | 3 Heroes s | UT (| <: | BD145144 Hernes ei | | 03093 TWA | 5444 ULZ/= | /4390 | 3657 | | Description | |

| TITLE JOURNAL | AUTHORS | REFERENCE | | ORGANISM | SOURCE | KEYWORDS | VERSION | ACCESSION | DEFINITION | LOCUS | I03657 | RESULT 1 |
|--|------------|--------------------|---------------|----------|----------|----------|--------------------|-----------|------------------------------------|-------------------------------|--------|----------|
| Immunologically reactive non-glycosylated amino acid chains of glycoprotein B of herpes virus types 1 and 2 Patent: US 464233-A 5 10-FEB-1987; | Person, S. | 1 (bases 1 to 798) | Unclassified. | Unknown. | Unknown. | • | I03657.1 GI:268613 | I03657 . | Sequence 5 from Patent US 4642333. | 103657 798 bp ss-DNA linear P | | |
| chain | | | | | | | | | | PAT 21-MAY-1993 | | |
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UL27=glycoprotein B [herpes simplex
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GBpath/UL27-glycoprotein B [herpes simplex virus type 1 HSV-1,

ANGpath, Genomic Mutant, 1478 nt]
                          Human herpesvirus 1
Human herpesvirus 1
Viruses; dsDNA viruses,
Alphaherpesvirinae; Simp
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Kostal,M., Bacik,I., Rajcani,J. and Kaerner,H.C.

Replacement of glycoprotein B gene in the herpes simplex virus type

Replacement of glycoprotein B gene in the herpes simplex virus type

1 strain ANGpath DNA by that originating from nonpathogenic strain

KOS reduces the pathogenicity of recombinant virus

KOS reduces the pathogenicity of recombinant virus
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261 c 254 g
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1 (bases 1 to 1857)

Bzik, D.J., Fox, B.A., DeLuca, N.A. and Person, S.

Nucleotide sequence of a region of the herpes simplex virus type 1
gB glycoprotein gene: mutations affecting rate of virus entry and cell fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein.
Human herpesvirus 1
Human herpesvirus 1
Viruses; dsDNA viruses,
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Original source text: HSV1 strain tsB5 DNA, clone pTBG-BS1. HSV1 strain tsB5 is a mutant of strain HFEM that is temperature dependent for virus growth, production of gB, and fusion of Vero and HEL cells. The syn and ts lesions of tsB5 are separable by recombination, the syn defect being located between 0.345 and 0.355 map units, and the ts defect being located between 0.360 and 0.368 map units. The rate of entry determinant of tsB5 is genetically separable from both the syn and ts lesions and is located between 0.350 and 0.360 map units, which is entirely within the glycoprotein B gene (0.348 to 0.366 map units).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yuhasz,S.A. and Stevens,J.G.
Glycoprotein B is a specific determ
type 1 neuroinvasiveness
Tylicol. 67 (10), 5948-5954 (1993)
                                                                                                                                                                                                                                                                                                                 Virology 137 (1), 185-190 (1984) 84301857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSV1 (mutant strain tsB5), glycoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93381796
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LRFADIDTVIHADANAAMFAGLGAFFEGMGDLGRAVGKVVMGIVGGVVSAVSGVSSFM
SNPFGALAVGLLVLAGLAAAFFAFRYVMRLQSNPMKALYPLTTKEL"
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MTKMQBVDEMLRSEYGGSFRSSDAISTTFTTMLTEYPLSRVULGDCIGKDARDAMDR
IFARRYNATHIKVGQPGYLANGGFLIAYQPLLSNTLAELYVREHLHCEQSRKPPNPTP
PPGRASANASVERIKTTSSIEFALGCTYNHIQRHVNDMLGRVAIAWCEQNHELTLM
NEARKLNPNAIASATVGRRVSARMLGDVMAVSTCVPVAADNVIVQNSMRISSRPGACY
SRPLYSFRYEDQGPLVEGQLGENNELRLTRDAIEPCTYGHRXYFTFGGGYVYFEEYAY
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/product="glycoprotein B"
/protein_id="AAP13961.1"
/db_xref="GI:30027723"
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|mol_type="genomic DNA"
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    OS Herpes simplex virus typel (HSV-1)
PN JP 1991218397-A/2
PD 25-SEP-1991
PF 21-JUN-1990 JP 1990161448
PR 22-JUN-1989 JP 89P 158238, 30-NOV-1989 JP 89P 308941 PI
FUJISAWA YURIO, HINUMA KUNIJI, ASAKAWA NAOKI, OTAKA SACHIKO PC
CO7K13/00, C12N1/19, C12N15/38, C12P21/02/A61K39/245, (C12N1/19, PC
C12R1:865),
PC (C12P21/02,C12R1:865);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
Canti-sense: No;
CC *source: strainsMiyama;
CC *source: clone=pHSB106 delta Tth;
FH Key Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: JP 1991218397-A 2 25-SEP-1991;
TAKEDA CHEM IND LTD
OS Herpes simplex virus type1 (HSV-1)
PN JP 1991218397-A/2
PD 25-SEP-1991
PD 25-SEP-1991
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(bases 1 to 2088)
Fujisawa, Y., Hinuma, K., Asakawa, N. and Otaka, S.
POLYPEPTIDE AND ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human herpesvirus 1
Human herpesvirus 1
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358 a 624 c 576 g 299 t
upstream of Sall site; map coordinate 0.360.
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*source: clone=pHSB106 delta Tth;
*source: clone=pHSB106 delta Tth;
Key Location/Qualifiers
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/db_xref="GI:330088"
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Pred. No. 3.3e+02;
Mismatches 0;
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gB of herpes simplex virus type1(HSV-1).
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                                                              Local Similarity
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 1917
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PC A61K39/245,C07H21/0
strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: strain=HG
CC *source: map_positi
FH Key
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OS helpes simp
PN JP 19851155;
PD 22-JUN-1985
PF 23-JUN-1984
PR 23-JUN-1983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SULANTEE, P.
NON-GLYCOSYLATED AMINO ACID CHAIN IMMUNOLOGICALLY REACTIVE TO GLYCOPROTEIN OF HERPES VIRUS 1 AND 2
Patent: JP 1985115529-A 2 22-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP 1985115529-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332
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TCACCACCGTCAGCACCTTC 1936
                        TCACCACCGTCAGCACCTTC
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                                                                                                                 481
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mat_peptide
                                                  100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                   A61K39/245, C07H21/04, C07K15/14, C12N15/00//C12P21/02; CC
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JP 1985115529-A/2
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23-JUN-1983 US 83 50698
                                                                                                                                                                                                                                              *source: map_position=0.386-0.348;
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                    source: strain=HG 52;
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                                                                                                                                                                                                                                                                       'source: clone=p52BXX;
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                                                                                                                                                                      /product='glycoprotein B of herpes simplex virus type 2'.
Location/Qualifiers
                                                                                                              /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
886 c 841 g 37
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Location/Qualifiers
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/db_xref≃"taxon:10298"
751 c 620 g
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/mol_type="genomic DNA"
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100.0%; Pred. No. 3.3e+02;
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/product='truncated
                                                              Score 20; DB 6;
Pred. No. 3.2e+02;
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RESULT 8
BD165793
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BD145144
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ACCESSION
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Matches 20
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                                                                   Herpes simplex virus 7
ISM Herpes simplex virus 7
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.

El (bases 1 to 2712)
Burke, R.L., Pachl, C. and Valenzuela, P.D.T.

Vaccine for use in the therapeutic treatment of HSV
Patent: JP 2002167398-A 2 11-JUN-2002;
CHIRON CORP
OS Herpes simplex virus 7
PN JP 2002167398-A/2
PN JP 2002167398-A/2
PN JP 2002167398-A/2
PN JP 2002167398-A/2
PR 11-JUN-2002
PP 11-JUN-2002
PP 12-SEP-2001 JP 2001277340
PR 20-CCT-1966 US
PR
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CHIRON CORP
OS HSV 9B1
PN JP 2002136297-A/4
PD 14-MAY-2002
PF 10-SEP-2001 JP 2001
PR 02-AUG-1990 US
PI RAE LYN BURKE, ROSE
PC C12N15/09, A61K38/0C
PC A61K37/02
CC Herpes simplex viru
PH Key
CDS
(1)
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Vaccine for use in the th
BD165793
BD165793.1 GI:27871605
JP 2002167398-A/2
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20; Conserv
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Burke, R.L. and Sekulovich, R.E.
Herpee simplex virus VP16 vaccine
Patent: JP 2002136297-A 4 14-MAY-2002;
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JP 20021362
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                                CDS
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02-AUG-1990 US 561.528
RAE LYN BURKE,ROSE E SEKULOVICH
C12N15/09,A61K38/00,A61K39/245,A61P31/12,C07K14/03,C12N15/00,
                                                    Vaccine for use in the therapeutic Location/Qualifiers
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Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
949 c 853 g 39
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location/Qualifiers
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100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0;
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BD165795
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DEFINITION
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VERSION
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SOURCE
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BD145143
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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                                                                                                ON Herpes simplex virus VP16 vaccine.

N BD145143.1 GI:27850901

JP 2002136297-A/3.

unidentified
M unidentified
M unidentified
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CHIRON CORP
OS Herpes simplex virus 7
OS Herpes simplex virus 7
PN JP 2002167398-A/4
PD 11-JUN-2002
PP 12-SEP-2001 JP 2001277340
PR 20-OCT-1986 US 921.213
PR 20
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Herpes simplex virus 7
Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 2712)
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1 (bases 1 to 2715)
Burke,R.L. and Sekulovich,R.E.
Herpes simplex virus VP16 vaccine
                                                                                    unclassified
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Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Herpes simplex virus
/mol_type="genomic DNA"
/db_xref="taxon:57277"
949 c 853 g 396 t
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                                                                                                                                                                                                                  Submitted (02-OCT-1998) Institute of Virology, Slovak Academy of Sciences, Dubravska cesta 9, Bratislava 842 46, Slovakia Location/Qualifiers
                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                 Herpes simplex virus 1 (HSV-1) strain comparison of mutations among strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human herpesvirus 1
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                                                                                                                                                                                                                                                                                            Kosovsky, J.,
                                                                                                                                                                                                                                                                                                                                                    Virus Genes 20 (1), 27-33 (2000)
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C12N15/09,A61K38/00,A61K39/245,A61P31/12,C07K14/03,C12N15/00,A61K37/02
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HSV gB2
JP 2002136297-A/3
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02-AUG-1990 US 561.528
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                                                          and cell membrane*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
938 c 886 g 40
product="glycoprotein B"
protein_id="AAF04615.1"
                            'codon_start=1
                                                                     function="essential for fusion between virion envelope
                                                                                      /gene="UL27"
                                                                                                                  'gene="UL27"
                                                                                                                                                             /organism="Human herpesvirus 1"
/mol_type="genomic DNA"
/strain="HSZP"
                                                                                                                                                                                                          1. .2715
                                          note="envelope glycoprotein; gB"
                                                                                                                                            db_xref="taxon:10298"
                                                                                                                                                                                                                                                                                         Vojvodova, A., Oravcova, I., Majorova, J.,
                                                                                                                                                                                                                                                                                                                                                                                                          Vojvodova, A., Oravcova, I.,
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AF295528
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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AF295528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein B
Unpublished
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1 (bases 1 to 2715)
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                                                                                                                                                                                                                   /gene="gB2"
/codon_start=1
/product="glycoprotein_B2"
/protein_id="AAK97852.1"
/db_xref="GI:15428576"
HRDDHETDMELKPAKVATRTSRGMHTTDLKYNPSRVEAFHRYGTTVNCIVEEVDARSV
YPYDERVLATGDFVYNSPFYGYREGSHTEHTSYAADR FRQVDGFYARDLTTKARATSP
TTRNLLTTPKFTVAMDWYPKRPAVCTMTKWQBVDEMLRAEYGGSFRFSSDAISTTFTT
NLTQYSLSRVDLGDCIGRDAREAIDRWFARKYNATHIKWGQPQYYLATGGFLIAYQPL
LSWTLAELYVREYMREQDRKPRNATPAPLREAPSANASVERIKTTSSIEFARLQFTYN
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LTRDALEPCTVGHRRYETFGGGYVYFESFYAYSHOLSRADITTVSTFIDLNITMLEDHE
FVPLEVYTRHEIKDSGLLDYTEVQRRNQLHDLFRADIDTVIHADANAAMFAGLGAFFE
GMGDLGRAVGKVVMGIVGGVVSAVSGVSSFMSNPFGALAVGLLVLAGLAAAFFAFRYV
MRLQSNPMKALYPLTTKELKNPTNPDASGEGEEGGDPDEAKLAEAREMIRYMALVSAM
                                                                                                                    /translation="MRGGGLICALVUGALVAAVASAAPAAPAAPAAGGVAATVAANG
GPASRPPPVBSPATTKARKRKKKPPERPEATPPDAVATVAACHATLAALLRBIKVE
NADAQPYVCPPPTGATVVQFBQPRKCPTRPEGQNYTEGIAVPFKENIAPXKFKATMY
KDVTVSQVMPGHRYSQPMGIFEDRAPVPFEEVIDKINAKGVCRSTAKYVRNNMETTAF
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TTPTTRUTEYPLSTVDLGDCIGKDARDAMDRIPARTYMATHIKYGQPQYYLANGGPLI
AYQPLLSNTLAELYVREHLREOSKKEPNPTPP PPGASANASVERIKTTSSIEFARLOF
TYNHIQRHVNDMLGRVAIAWCELQNHELTLWNEARKLNPNAIASATVGRRVSARMLGD
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ATMYXDDVTVSQVMFGHRYSQMGIFEDBAFVENTUDKINAKGVCRSTAKYVRNI
ATMYXDDVTVSQVMFGHRYSQMGIFEDBAFTDLKYNPSRVBAFHRYGTTVNCIVEBV
ETTAFHRDDHETDMELKPANJATRTSSGMHTTDLKYNPSRVBAFHRYGTTVNCIVEBV
DARSVYPYDEFVLATGDFVYMSPFYGYREGSHTEHTSYAADRFKQVDGFYARDLTTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EHTEHKAKKKGTSALLSAKVTDMVMRKRRNTNYTQVPNKDGDADEDDL"
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                                                                                                                                                                                                                                                                                                                                        /gene="gB2"
|. .2715
                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10310"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      'strain="G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Human herpesvirus 2"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (12-AUG-2000) Department of Biology, Konkuk University,
Mg, Kwangjin-gu, Seoul 143-701, Korea
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Pred. No. 3.2
D; Mismatches
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-OCT-2000) Microbiology-Immunology, Northwestern University Medical School, 320 E. Superior Ave., Ward 6-241, Chicago, IL 60611, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 2715)
Pertel, P.E., Fridberg, A., Parish, M.L. and Spear, P.G. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertel, P.E., Fridberg, A., Parish, M.L. and Spear, P.G. Cell fusion induced by herpes simplex virus glycoproteins and gH-gL requires a gD receptor but not necessarily hepar
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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Human herpesvirus 1 strain KOS
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DALEPCTVGHRRY PI FGGGYVY PEBYAYSHQLGRADVTTVSTET DLNI TWLEDHBI VP
LEVYTRHEI KDSGLLD YTEVQRRNQLHDI DTVI RADDANAMPAGLCAF PEGMG
DLGRAVGKVVMGVVGGVVSAVSGVSSFMSNPFGALAVGLLVLAGLVAAPFAFRYVLQL
QRNPMKALY PLTTKELKTSDPGGYGGEGEEGAEGGGFDEAKLAEAREM RYMALVSAM
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1 (bases 1 to 2715)

Holland T. C. and Saharkhiz-Langroodi, A.

Direct Submission
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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ERTEHKAKKKGTSALLSAKVTDMVMRKRRNTNYTQVPNKDGDADEDDL"
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/strain="ANG path"
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                              Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human herpesvirus 1
Human herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 2809)
Ling, J. -Y., Chen, T. -M. and Stroop, W.G.
A viral genetic element involved in a rabbit model of herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
2 (bases 1 to 2809)
2 (bases 1 to 2809)
Ling,J.-Y., Chen,T.-M. and Stroop,W.G.
Direct Submission
Direct Submission
Submitted (24-APR-2000) Ophthalmology, Mail Slot 523, University of Arkansas for Medical Sciences, 4301 West Markham, Little Rock, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human herpesvirus 1 glycoprotein B (UL27) gene, complete cds. AF259899
AF259899.1 GI:7839508
                                                                                                    TCACCACCGTCAGCACCTTC 20
                                                                                                                                                                                                                                                                                                                                             536
                                                                                                                                                                                                   100.0%; Score 20; DB 14; ilarity 100.0%; Pred. No. 3.2e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  /translation="mrqqapargcrwprywallgitlgylvasaapssgrtpgyaaat"
/bransgapatbarpapaggcrwprywallgitlgylvasaapssgrtpgyaaat
/branggapatbarpapaggrypregrakkyrpppggadvatvaaghatlaehlr
DIKAKNIDANPYVCPPPTGATVVQFEQFREGTRPBEGQNYTEGIAVVFKENIAPYKFK
ATMYYKDVTVSQVWFGERYSQFWGIFEDRAPVPEBVIDKINAKGVCRSTAKYVENNL
ETTAFHRDDHETDMELKPANAATRISRGWHTTDLKYNPSRYDAFHRYGTYVGNUCIVEBV
DARSVYPYNBFYLATGDFYYMSPFYGYREGSHTEHTSYAADRFKQVDGFYARDLTTKA
RATAPTTRNLLTYPKFYVAWDMVPKRPSYCTMTKWQBVDEMLRSSYGGSFRFSSDAIS
TTFTTNLTEYPLSRVDLGDCIGKDARDAMDRIFARXHANIFIKYGQPQYYLANGGFLI
AYQPLLSNTLAELYVREHLREGSRKPBNPTPPPPBASANASVERIKTTSSIEFARLQF
TYNHIGRYNINGLGRVAIAWCEGLQNHELTLWNEARKLNENAIASVERIKTTSSIEFARLQF
TYNHIGRYNINGLGRVAIAWCEGLQNHELTLWNEARKLNENAIASVERIKTTSSIEFARLQF
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TYNHIGRYNINGLGRVAIAWCEGLQNHELTLWNEARKLNENAIASVERIKTTSSIEFARLQF
TYNHIGRTYNDHAGRTSTAWCHELR
LTRDAIEPCTVGHRRYFTFGGGYYFEBYAYSHQLSRADITTVSTFIDLNITMLEDHE
FVPLEYYTRHEIKDGGLLDYTEYGRRNQLHDLRFADIDTVIHADAAMPGGLAGAFFE
GMGDLGRAVGKVUNGTVGGVVSAVSGVSSFMSNFFGALVSALAEARMIRYMALVSAM
EHTEHKAKKKGTSALLSAKVTDMVMKKRATNTYTQVPNKDSDADEDDL"
36 a 974 c 883 g 416 t
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38. .2752
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/mol type="genomic DNA"
/strain="+GC"
/db xref="taxon:10298"
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/product="glycoprotein_B"
/protein_id="AAF70301.1"
/db_xref="GI:7839509"
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                                                                                                                                                                                                                                                         Length 2809;
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Sequence encoding
HSV-2 strain SB5 C
Human herpesvirus
DNA encoding T. ch

Transglutaminase (
DNA encoding T. ch
Complete nucleotid
Plant D-like cycli
Plant SDF polynucl
Arabidopsis thalia
Drosophila melanog
Human foetal liver
Probe #2089 for ge
Human bone marrow
Human bone marrow
Human liver single
Human foetal liver
Aspergillus oryzae
DNA encoding novel
Human olfactory re
Human GREC-33 CDN
DNA encoding novel
Human GCREC-33 CDN
DNA encoding a hum
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Glycoprotein B (gB Glycoprotein B (gB Herpes simplex vir Sequence of Herpes DNA fragment encod

Recombinant herpes
HSVgB gene. Herpe
Herpes simplex vir
Sequence of Herpes

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Result
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                             Score
            00000000
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Match Length DB
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Gapop 10.0 , Gapext 1.0
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
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Sequence encoding
HSV-2 strain SB5 C
HSV surface antige
Herpes simplex vir
                                                                                                                  Truncated HSVgB ge
HSV-2 strain SB5 C
Herpes Simplex Vir
Herpes Simplex Vir
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| E) TAKEDA | .JUN-1989 .JUN-1989 | JUN-1990 | SEP-1991 | 397- | | es simplex | ine; | cated HS | MAR-2003 JAN-1992 | 4479; | .4479 st | | • | . 60 | ٠. | ט פּע | ٠ | ტ : | , 0 | 16.8 | υ. | ο : | ν. Ο | 6 | ٠, | 7. | 17.4 | | 00 0 | œ . | ່ພ | 200 | 20 | 20 | 200 | 20 | 20. | 20 | 20 |
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| MIND | P-0308 P-0158 P-0161 | P-0161 | | | cation .2088 tag= | us. | 88. | ne. | ted) | | DNA; | | | | 1485 | 1242 | 9 | 4 | υo | 780 | 9 | | ח מ | | a c | | 658 | 9 | N | 9 8 | 74 | 721 | 200 | 47 | 47 | 4.7 | 47 | 4.6 | 6 |
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| | | | | | lifiers | | | | | | BP. | ALIGNMENTS | T1917 | 6159 | 6159 | 8731 | 9072 | 792 | 7741 | AAS81093 | 5712 | 2716 | 0214 | 2362 | 1700 | 5199 | 7848 | 3016 | 293 | 293 | 2551 | 6217 | 38 | 8060 | 926 | 4849 | | 14 | 1890 |

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AC AAV62158;
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XX BSV-2 stri
XX HSV-2 stri
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Best Local S
Matches 20
     This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 st SBS (deposited as ATCC VR-2546), is designated Contig ID 14, and es a HSV-2 protein. The protein can be used for the treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2088 BP; 417 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence encodes a truncated form of the HSVgB polypeptide. The recombinant protein can be used to prepare vaccines for prophylaxis of HSV infection and for use in diagnostic kits. See also AAQ14478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 7; 24pp; Japanese.
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P-PSDB; AAR14666.
                                                                                                                                                                                                                                                                  09-JUN-1997;
04-NOV-1996;
                                                                                                                                                                                                                                                                                                          31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSV-2 strain SB5; immunological response induction; antiviral identification; viral protein inhibitor; a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cheaply and safely.
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                                                                                                               Herpes simplex virus type-2 sequences - useful in, and treatment of infection or inducing immunologica
                                                                                                                                                                     WPI; 1998-286847/25.
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                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCACCACCGTCAGCACCTTC 1923
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                                                                                                                                                                                              Dabrowski-Amaral CE,
Leary JJ;
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96US-0030279.
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XX PP 10-E
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XX YP 20-C
XX AND
PT 10-E
XX WPI
DR P-PI
XX MPI
XX AND
PT 10-E
XX AND
PT 10
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Best Local S
Matches 20
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Matches
                                                                                     Query Match
                                                                                                                                                                      corresponding to that occurring in glycoprotein B of HSV-1 or HSV-2 virus which is antigenic to HSV-1 of HSV-2, which contains no more than 750 AA residues, and which includes AA residues 135-649 inclusive is claimed. It can be used to produce vaccines for prophylaxis and treatment of HSV-1 and HSV-2. See AAN71399 for the HSV-2 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevention of disease, to induce an immunological response in to identify inhibitors, activators or novel antivirals. Antago the proteins can be used to inhibit a viral polypeptide. The D or a vector containing it can also be used to induce an immuno response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant and 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein;
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                                                                                                                                Sequence 2712 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid chain of glyco:protein recombinant and used for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Person
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes Simplex Virus-1 gB from pKBXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
30-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAN71303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1987-056354/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-FEB-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAN71303 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PERS/) PERSON
                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP71135
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                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prophylaxis; treatment; Herpes Simplex Virus-1;
tein; gB; ss.
                                                                                                                                                                                                                                                                                                                                                                          Table 2; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2645 BP; 404 A; 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCACCACCGTCAGCACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACCACCGTCAGCACCTTC
  TCACCACCGTCAGCACCTTC
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(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B4US-0622496
                                                                                                                                519 A; 945 .C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type 1
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                                          Score 20; DB
Pred. No. 24;
); Mismatches
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO;
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                                                                                                                                <u>ن</u>
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                                                                                                                                  397 T;
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                                                                                       B
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                                                                                                                                  2 other;
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                                                                                     Length 2712;
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                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           prepd. as virus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2645;
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                                               Gaps
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RESULT 4
AAN71399
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Best Local
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                                                                                                                                                                                                                                                         A pure non-glycosylated amino acid (AA) chain comprising a sequence corresponding to that occurring in glycoprotein B of HSV-1 or HSV-2 virus which is antigenic to HSV-1 of HSV-2, which contains no more than 750 AA residues, and which includes AA residues 135-649 inclusive is claimed. It can be used to produce vaccines for prophylaxis and treatment of HSV-1 and HSV-2. See AAN71303 for the HSV-1 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; prophylaxis; treatment; Herpes Simplex Virus-1;
glycoprotein; gB; ss.
         Vaccine; glycoprotein B; ss
                            Sequence encoding the type 2 (HSV-2).
                                                                             AAN50517;
                                                                                                AAN50517
                                                                                                                                                                                                                            Sequence 2724 BP; 494 A; 911 C; 854 G;
                                                                                                                                                                                                                                                                                                                                                         Example; Table 2; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Amino acid chain of glyco:protein B of HSV-1 and 2 - prepd. as recombinant and used for vaccines for herpes simplex virus types
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Person
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes simplex virus type 2 HG52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes Simplex Virus-2 gB from p52BXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
30-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN71399 standard; DNA; 2724 BP.
                                                          21-NOV-1991
                                                                                                                                                                                                                                                                                                                                      'N' indicated nucleotide to be determined (corresp. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PERS/) PERSON
                                                                                                                                                                                               Local
                                                                                                                                                 1991
                                                                                                                                                                                                                                                                                                                                                                                                                    1987-056354/08.
DB; AAP71136.
                                                                                                                                                                                                                                                                                                                              of HSV-1 gB).
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                                                                                                                                                                                                Similarity
                                                                                                                                                          TCACCACCGTCAGCACCTTC
                                                                                               standard;
                                                                                                                                                TCACCACCGTCAGCACCTTC
                                                                                                                                                                                                                                                on 25-MAR-2003 to correct
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
                                                          (first
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                                                                                               DNA;
                                                         entry)
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                                      glycoprotein
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                                                                                                                                                                                              Score 20;
Pred. No.
                                                                                                                                                 2010
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                                                                                                                                                                                                                                                PR field.)
                                      (gB) of Herpes simplex virus
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••
                                                                                                                                                                                                                             75 other;
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                                                                                                                                                                                                         Length 2724;
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                                                                                                                                                                                                                                                                                                                                       residues
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AAV62146
ID AAV6
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Matches
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23-JUN-1983;
20-JUN-1984;
         09-JUN-1997;
04-NOV-1996;
                                                                                                                                                       HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
                                                                                                                                                                                                         07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2727
                                      31-OCT-1997;
                                                                                                                                     Herpes
                                                                                                                                                                                     HSV-2 strain SB5 Contig ID 91 DNA sequence.
                                                                                                                                                                                                                             AAV62146;
                                                                                                                                                                                                                                              AAV62146 standard; DNA; 2841 BP
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                                                                            WO9820016-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Person
                                                                                                                                                                                                                                                                                                1994
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                                                                                                                                    simplex virus type 2.
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         97US-0049018
96US-0030279
                                      97WO-US20016.
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/*tag= a

Location/Qualifiers

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The inventors claim a non-glycosylated amino acid chain comprising a sequence corresponding to that occurring in glycoprotein B of HSV-1 or HSV-2. Preferably, when the chain comprises a sequence corresp. to that occurring in glycoprotein B of HSV-2, it contains 4-750 AA residues. The chain esp.has a molecular wt. of 65000 daltons and includes AA residues 165-629 from the HSV-2 glycoprotein B sequence.
                                                                                                                                                                                                                             New amino acid chains of glyco-protein B of herpes simplex virus - prepd. by recombination DNA methods for use in vaccines
                                                                                                                                                                                                    Disclosure; Table 2, Page 35-35C; 40pp; English.
                                                                                                                                                                                                                                                                  WPI; 1985-039636/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus type
                                                                                                                                                                                                                                                                                                                (PERS/) PERSON S.
                                              Local Similarity
nes 20; Conserv
            TCACCACCGTCAGCACCTTC 20
TCACCACCGTCAGCACCTTC 2013
                                               Conservative
                                                                                            BP; 493 A; 913 C; 855 G;
                                                                                                                                                                                                                                                                                                                                        84US-0622496,
                                                                                                                                                                                                                                                                                                                                                   83US-0532996.
83US-0506986.
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                                                        100.0%;
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                                              0;
                                              Score 20; DB
Pred. No. 24;
0; Mismatches
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6
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RESULT 7
AAQ14455
ID AAQ1
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Matches 20
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                                                                                                                                                                                                                                           CDS
   Claim 6; Fig 8; 16pp; Japanese.
                                     Polypeptide for herpes simplex virus vaccine prodn. -culturing transformant of recombinant DNA coding fused
                                                                                                                              30-NOV-1989;
29-NOV-1990;
                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
21-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                     AAQ14455 standard; DNA; 2925
                                                                       P-PSDB; AAR14680
                                                                                  WPI; 1991-329235/45.
                                                                                                                                                               29-NOV-1990;
                                                                                                                                                                                     27-SEP-1991.
                                                                                                                                                                                                            JP03220200-A
                                                                                                                                                                                                                                                                           Herpes
                                                                                                                                                                                                                                                                                                  Herpes
                                                                                                                                                                                                                                                                                                                        HSV gurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 284-285; 748pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpes simplex virus
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                                                                                                         (TAKE )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pes simplex virus type-2 sequences - treatment of infection or inducing i
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2012
                            Burface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCACCACCGTCAGCACCTTC 20
                                                                                                                                                                                                                                                                            simplex virus
                                                                                                                                                                                                                                                                                                simplex virus; vaccine;
                                                                                                        TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dabrowski-Amaral CE,
Leary JJ;
                                                                                                                                                                                                                                                                                                                        antigens gB/gD fusion protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                          antigen
                                                                                                                              89JP-0308942.
90JP-0325474.
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Pred.
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    useful in, e.g. prevention
immunological response in

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                                      fused
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          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The DNA sequence encodes a fusion protein comprising herpes simplex virus (HSV) surface antigens gB and gD. This fusion protein shows the same physiological activity as surface antigen prepd. from HSV infected cells. It can be used in a vaccine for the prevention of HSV infection.
                                                                   Virus infections. The vaccine is mafe in use carcinogenic gene, as with prior vaccines. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                     The gene encodes a gB glycoprotein which is useful for the production of vaccines conferring protection against herpes simplex virus infections. The vaccine is safe in use and does not contain a
                                                                                                                                                                      Recombinant DNA containing herpes simplex virus gene or fragment useful in transformant yeast for prodn. of high purity herpes simplex virus glycoproteins for use in protective vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
31-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2925 BP; 579 A; 1061 C; 848 G; 437 T; 0
                                             Sequence 3098
                                                                                                                                                   Disclosure; Fig. 6; 53pp; English.
                                                                                                                                                                                                                                                          Nozaki
                                                                                                                                                                                                                                                                                                                                                                                    EP170169-A.
                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSV; gb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus glycoprotein gB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAN60195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN60195 standard;
                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                     20-JUL-1984;
11-DEC-1984;
                                                                                                                                                                                                                                                                                                                                       19-JUL-1985;
                                                                                                                                                                                                                                                                                                                                                              05-FEB-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                               (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1904
                                                                                                                                                                                                                                   1986-036935/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        simplex virus
                                                                                                                                                                                                                        AAP60244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCACCACCGTCAGCACCTTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCACCACCGTCAGCACCTTC 1923
                                                                                                                                                                                                                                                          Makizumi K,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                            BP;
                                                                                                                                                                                                                                                                                                     84JP-0151766.
84JP-0262465.
                                                                                                                                                                                                                                                                                                                                        85EP-0109042
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 257..2966
                                            586 A; 1070 C; 959 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 3098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
          100.0%; Score 20; 100.0%; Pred. No.
                                                                                                                                                                                                                                                          Kino
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                         Eto,
                                                                                                                                                                                                                                                          Ή
                                             483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB
                      DB
                                                                                                                                                                                                                                                          Ohtomo
                                             T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                     Length 3098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other;
                                               other
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                                                                                                                                                                                                                                                           z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٥,
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Mismatches

0

Indels

0

Gaps

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RESULT 10
AAQ14478
ID AAQ14
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AAN70681
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                                                                                                                      Query Match
Best Local S
Matches 20
                                                                                                                                                                                         The gene encoding HSV gB is cloned into E.coli. To increase the efficiency of expression, the gene encoding the C-terminal region of gB, which is very hydrophobic, is removed and the remaining gene is cloned into an expression vector. The vector is composed of pBR322, SV40 early promoter and the HSV gB gene.

The construct is useful for the production of a good antigen for a HSV vaccine.

(Updated on 10-MAR-2003 to add missing of field to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
10-MAR-2003
30-APR-1991
          AAQ14478;
                             AAQ14478 standard;
                                                                                                                                                              Sequence 3461 BP; 666 A; 1188 C; 1041 G; 566 T; 0 other;
                                                                                                                                                                                                                                                                                    Disclosure; Fig 3(1-3); 13pp; Japanese.
                                                                                                                                                                                                                                                                                                        Recombinant DNA contg. herpes simplex virus gene - is integrated E.coli plasmid vector, contg. incorporated promoter region for animal cells, giving antigen.
                                                                                                                                                                                                                                                                                                                                                           WPI; 1987-183377/26.
                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP62115288-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes simplex virus; E.coli; plasmid; vector; promoter; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN70681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN70681 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; glycoprotein; HSV
                                                                                                                                                                                                                                                                                                                                                                               (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
                                                                                2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2244
                                                                                                                      20;
                                                                                                                                 Similarity
                                                                                           TCACCACCGTCAGCACCTTC
                                                                                                                                                                                 on 10-MAR-2003 to add missing OS field.) on 25-MAR-2003 to correct PA field.)
                                                                               TCACCACCGTCAGCACCTTC 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCACCACCGTCAGCACCTTC 2263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCACCACCGTCAGCACCTTC
                                                                                                                    100.0%; silarity 100.0%; silarity 100.0%; sometime of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      herpes simplex virus gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   85JP-0255971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
254..2962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= HSV_gB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gB;
                              ₽₽
                                                                                                                     Score 20; DB 8; Length 3461;
Pred. No. 25;
; Mismatches 0; Indels
                                                                                                 20
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Query Match
Best Local Similarity
Matches 20; Conserva
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22-JUN-1989;
21-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                  The sequence encodes the HSVgB polypeptide. The recombinant profession esp. truncated forms of it, can be used to prepare vaccines prophylaxis of HSV infection and for use in diagnostic kits. See also AAQ14479.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                      Herpes simplex virus; HSV; type I; type II; glycoprotein B; vaccine; membrane protein; virus-specific glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                             Sequence 3465 BP; 666 A; 1194 C; 1044 G; 561 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSVgB polypeptide(s) obtd. by recombinant DNA techniques - useful as vaccines against HSV and in diagnosis, can be procheaply and safely.
TATA_signal
                                                                       Herpes simplex virus type 1.
                                                                                               transmembrane
                                                                                                                                           Herpes simplex virus type 1 glycoprotein B encoding DNA
                                                                                                                                                                   26-FEB-1998 (first entry)
                                                                                                                                                                                             AAT93650;
                                                                                                                                                                                                                  AAT93650 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 1; 24pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR14665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-328397/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP03218397-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine; antigen; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
23-JAN-1992
                                 CAAT_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1991.
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                                                                                                                                                                                                                                                                              2241
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                                                                                                                                                                                                                                                                                          1 TCACCACCGTCAGCACCTTC 20
                                                                                                                                                                                                                                                                              TCACCACCGTCAGCACCTTC 2260
                                                                                                                                                                                                                                                                                                                              Conservative
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(first entry)
                                                                                            anchor region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89JP-0308941.
89JP-0158238.
90JP-0161448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90JP-0161448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251..2965
/*tag= a
/*tag= a
/note= "putative"
125..131
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                   3471
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                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                     ΒP
                                                                                                                                                                                                                                                                                                                                         Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                     DB 12;
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                                                                                                                                                                                                                                                                                                                                                                             0 other;
                                                                                                                                                                                                                                                                                                                                                   Length 3465;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            produced
                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
les for
                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 12
AAN80907
ID AAN80
XX AAN80
XX AAN80
XX AAN80
XX BEQUE
XX BEQUE
XX Vacci
XX Vacci
XX Verepe
XX Verepe
XX Verepe
XX Key
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Best Local Similarity
                                                                                                                                                                                                                                                                           Matchee
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06-APR-1984;
20-SEP-1990;
21-DEC-1992;
                                                                                                                                                                                                                                                                                                                                            The present sequence is from the Herpes simplex virus (HSV) type I strain Patton and encodes a glycoprotein B. HSV is a double stranded virus packaged within an icosohedral nucleocapsid enveloped within a membrane. The membrane includes a number of virus-specific glycoproteins, with glycoprotein B being one of the most abundant. Glycoprotein B from both HSV type I and type II are cross reactive. New vaccines comprising recombinantly produced glycosylated glycoprotein B that has a deletion of at least part of the transmembrane anchor region, in combination with a carrier and an adjuvant have been produced. The vaccines are used for immunising humans against HSV (HSV type 1) by vaccination before or after primary infection with HSV.
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                                                                                                     25-MAR-2003
09-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccines against herpes simplex virus infection - recombinant HSV glycoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyA_signal
                               Herpes
                                                     Vaccine; herpes simplex virus; therapy; ss
                                                                             Sequence
                                                                                                                                        AAN80907;
                                                                                                                                                                AAN80907
                                                                                                                                                                                                                                                                                                                         Sequence 3471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4A-F; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW34552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-372022/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1997.
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                                                                                                                                                                                                                                                                          20;
                               simplex virus
                                                                                                                                                                                                                                          TCACCACCGTCAGCACCTTC 20
                                                                               0f
                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pachl C,
                                                                                                                                                                                                                                                                        Conservative
                                                                             Herpes simplex virus (HSV) glycoprotein B
                                                                                                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                        BP; 639 A; 1201 C; 1069 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86US-0921730.
84US-0597784.
90US-0587179.
92US-0993415.
93US-0138717.
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3166..3173
/*tag= d
/note= "putative"
3409..3416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "putative"
309..3023
      Location/Qualifiers
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                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                    100.0%; Score 20; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Valenzuela
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                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                   DB
25;
                                                                                                                                                                                                                                                                                                                        562 T; 0 other;
                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                Length 3471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               containing
                                                                                                                                                                                                                                                                           Indels
                                                                            (gB)
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                                                                                                                                                                                                                                                                        0,
                                                                                DNA.
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RESULT 13
AAQ48496
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Best Local (
                                                                                                                                                                                                                    25-MAR-2003
29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                             Prepn. of recombinant gB and gD is described in WO88504587. The amino acid sequence and DNA sequence for gB 1 presented in RAP80914 and AAN80907 differ from that originally presented in Table 1 of International Publication No. WO 85/04587. The DNA sequence in Table 1 contains an error in that an additional nucleocide (G) is listed at position 607 which resulted in a shift in reading frame relative to AAN80907 from which this nucleotide has been deleted.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                       CDS
                                                                                                                                                      Glycoprotein; gB1; gB2; herpes simplex virus; HSV-1; HSV-2; flanking; initiation; termination; transcription; translation; regulatory sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burke LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SdC
06-APR-1984;
20-OCT-1986;
                                                                                                                                   Herpes
                                                                                                                                                                                                 Glycoprotein
                                                                                                                                                                                                                                                                         AAQ48496 standard;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3472 BP; 639 A; 1202 C; 1068 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Fig 4; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine for treatment of herpes simplex virus - contains
recombinant HSV glyco:proteins B and D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-1987;
20-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO8802634-A.
                                                    14-SEP-1993.
                                                                                                                                                                                                                                                     AAQ48496;
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                              20-SEP-1990;
                                                                       US5244792-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                            2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1988-119368/17.
                                                                                                                                    simplex
                                                                                                                                                                                                                                                                                                                                                1 TCACCACCGTCAGCACCTTC 20
                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                            TCACCACCGTCAGCACCTTC 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pachl C,
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                 B (gB1).
                                                                                                                                                                                                                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87US-0079605.
86US-0921213.
                                                                                                                                     virus 1 strain Patton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87WO-US02709
84US-0597784.
86US-0921730.
                               90US-0587179
                                                                                                     Location/Qualifiers 309..3023
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                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                         3472
                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                    Score 20; DB
Pred. No. 25;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                             563 T;
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Best Local
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                                                                                           06-APR-1984;
20-OCT-1986;
2Q-SEP-1990;
                     WPI; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA constructs for expressing a glycosylated polypeptide in a eukaryotic host cell comprises (1) an oligonucleotide sequence (0S) free of natural flanking sequences, encoding glycoprotein B (gB) of HSV, or its fragments, and (2) 5' initiating and 3' terminating transcriptional and translational regulatory sequences flanking OS, at least one of these sequences not being from HSV. The HSV-1 and HSV-2 sequences are given in AAQ48496 and AAQ48497 respectively. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                      20-SEP-1990;
                                                                                                                                                                               US5244792-A
                                                                                                                                                                                                                                          Herpes simplex virus 2 strain 333.
                                                                                                                                                                                                                                                               regulatory sequence; ss.
                                                                                                                                                                                                                                                                          flanking;
                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                       Glycoprotein B (gB2).
                                                                                                                                                                                                                                                                                                                             25-MAR-2003
29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                             AAQ48497;
                                                                                                                                                                                                                                                                                                                                                                               AAQ48497 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA construct for expressing HSV glycosylated polypeptide useful for vaccinating against HSV-1 and -2 infections
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P-PSDB; AAR41778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-SEP-1990;
DNA construct for expressing HSV glycosylated polypeptide
                                                                                                                                                           14-SEP-1993.
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                                                                        (CHIR ) CHIRON CORP
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                     1993-302641/38
DB; AAR41779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCACCACCGTCAGCACCTTC 20
                                                                                                                                                                                                                                                                        initiation; termination;
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                                                   Pachl C,
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                                                                                                                                                                                                                                                                                                                            (updated)
                                                                                                                                                                                                                                                                                   gB1; gB2; herpes simplex virus; HSV-1; HSV-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 639 A; 1202 C; 1069 G; 562 T;
                                                                                           84US-0597784.
86US-0921730.
90US-0587179.
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                                                                                                                                                                                                 Location/Qualifiers 309..3023 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                         transcription;
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ID AAT93651
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AC AAT93
AC AAT94

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Best Local S
Matches 20
                                                                                                                                                                                        20-OCT-1986;
06-APR-1984;
20-SEP-1990;
21-DEC-1992;
18-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus; HSV; type I; type II; gl membrane protein; virus-specific glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA constructs for expressing a glycosylated polypeptide in a eukaryotic host cell comprises (1) an oligonucleotide sequence (OS) from of natural flanking sequences, encoding glycoprotein B (gB)
WPI; 1997-372022/34.
P-PSDB; AAW34553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT93651 standard; DNA; 3473 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5648079-A.
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                                                                                                                                       (CHIR ) CHIRON CORP
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mes 20; Conserv
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                                                                                Pachl C,
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                            86US-0921730.
84US-0597784.
90US-0587179.
92US-0993415.
93US-0138717.
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/note= "putative"
309..3023
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2744..2751
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Pred. No. 25;
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Vaccines against herpes simplex virus infection - containing

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Search completed: September 16, 2003, 18:36:57 Job time: 102.198 secs
                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 20; DB 18; Length 3473; Best Local Similarity 100.0%; Pred. No. 25; Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is from the Herpes simplex virus (HSV) type 2 strain 33 and encodes a glycoprotein B. HSV is a double strained virus packaged within an icosohedral nucleocapsid enveloped within a membrane. The membrane includes a number of virus-specific glycoproteins, with glycoprotein B being one of the most abundant. Glycoprotein B trom both HSV type I and type II are cross reactive. New vaccines comprising recombinantly produced glycosylated glycoprotein B that has a deletion of at least part of the transmembrane anchor region, in combination with a carrier and an adjuvant have been produced. The vaccines are used for immunising humans against HSV (HSV type 1 or HSV type 2) by vaccination before or after primary infection with HSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4A-F; 33pp; English.
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Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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   seq length: 0 seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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   569978 seqs, 220691566 residues
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             Length
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1 US-08-164-839-7
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1 US-08-164-839-9
1 US-08-164-839-9
1 US-09-142-623-10
1 US-09-142-623-10
1 US-09-142-623-2
2 US-09-142-623-2
3 US-09-133-840A-1
1 US-09-252-991A-793
1 US-09-252-991A-12830
1 US-09-252-991A-12830
1 US-09-252-991A-12830
1 US-09-252-991A-12830
1 US-09-252-991A-12830
1 US-09-252-991A-12831
1 US-09-252-991A-12842
1 US-09-252-991A-13319
1 US-09-252-991A-13319
1 US-08-942-4647A-4
1 US-08-941-991-3
1 US-09-252-991A-13319
1 US-08-941-991-3
1 US-09-252-991A-13319
1 US-08-941-991-3
1 US-09-252-991A-13319
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       Sequence 13, Appl
Sequence 13, Appl
Patent No. 5244792
Patent No. 5244792
Patent No. 5244792
Patent No. 5244792
Sequence 7, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 10, Appli
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Sequence 1, Appli
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RESULT 1
US-08-804-439A-13
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; Sequence 13, Applica
; No. 6015565
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APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marrix L.
APPLICANT: Strand, Kurt
TITLE OF INVENTION: GLYCOPROTEIN B
TITLE OF INVENTION: SUBFAMILY OF HE
NUMBER OF SEQUENCES: 113
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                                                            Query Match
Best Local Similarity
Matches 20; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00/804,439A
FILING DATE: February 21, 1997
CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 09176/004001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
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ADDRESSEE: Fish & Richardson P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
COUNTRY: USA
ZIP: 92037
                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 678-5099
TELEX:
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                                                                                                                                                                                  TOPOLOGY:
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US-09-453-702B-39
US-09-676-610B-24
US-09-877-177A-10
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-298-886-20
US-08-148-708-4
US-09-313-294A-7433
US-09-313-294A-738
US-09-313-294A-738
US-09-313-294A-738
US-09-313-294A-738
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US-09-313-294A-738
US-09-313-294A-7389
US-09-252-991A-2369
US-09-252-991A-2369
US-09-252-991A-2833
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US-09-252-537-22
US-09-252-537-22
US-09-252-537-28
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US-09-252-537-28
US-09-252-537-28
US-09-252-537-28
US-09-252-537-28
US-09-252-537-28
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                                                            Score 20; DB
Pred. No. 6;
0; Mismatches
                   20
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HERPES VIRUSES
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                                                                                                            Length 2713;
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Sequence 39, Appl
Sequence 24, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 7433, Appli
Sequence 6329, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 2369, Ap
Sequence 2369, Ap
Sequence 2375, App
Sequence 2833, Ap
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Sequence 39, Appl
Sequence 24, Appl
Sequence 10, Appl
                                                                 0
                                                                 Gaps
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TCACCACCGTCAGCACCTTC

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RESULT 3
5244792-1
; PATENT NO. 5244792
; APPLICANT: BURKE, RAE L.; PACHL,
; TITLE OF INVENTION: EXPRESSION (
5244792-1
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US-08-720-229-13
                                  SEQ ID NO:1:
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Best Local 9
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 bacc
TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/720,229
FILING DATE: 26-SEP-1996
CLASSIFICATION: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 29938-20002.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
                                                                                                                                                                           FROM HERPES SIMPLEX VIRUS NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

ODERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 921,730
FILING DATE: 20-OCT-1986
APPLICATION NUMBER: 597,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESSE: MOTTIBON & FOBTBUEF
ADDRESSEE: MOTTIBON & FOBTBUEF
STREET: 755 Page Mill Road
             LENGTH: 3472
                                                   FILING DATE: 06-APR-1984
                                                                                                                                         APPLICATION NUMBER: US/08/587,179
FILING DATE: 20-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV TLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
                                                                                                                                                                                                                                                                                                                                                                  1988
                                                                                                                                                                                                                                                                                                                                                                                                  1 TCACCACCGTCAGCACCTTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
DEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                  TCACCACCGTCAGCACCTTC 2007
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Pred. No.
                                                                                                                                                                                                                                    OF RECOMBINANT GLYOPROTEIN
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US-08-164-839-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Patent No. 5244792
; APPLICANT: BURKE, RAE L
; TITLE OF INVENTION: EXPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5244792-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: YASUEDA
APPLICANT: NAKANIS
APPLICANT: NOTOKI,
APPLICANT: NAGASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
APPLICATION NUMBER: 08/004,729
APPLICATION NUMBER: 08/004,729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/58
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 921,730
FILING DATE: 20-OCT-1986
APPLICATION NUMBER: 597,784
FILING DATE: 06-APR-1984
                                                                                                                                                                                                                                                                STREET: 1/55
STREET: Arlington
CITY: Arlington
STATE: Virginia
STATE: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
                FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 55145731
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED TITLE OF INVENTION: FROM FISH
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAKANISHI, KAZUO
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                                                                                                                                                                                                                                                                                                                                                                OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAE L.; PACHL, CAROL; VALENZUELA, N: EXPRESSION OF RECOMBINANT GLY
                5514573man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20;
100.0%; Pred. No.
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                                                                                                                                       US/08/164,839
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                                                                                                                                                                          Version
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RESULT 6
US-08-583-799-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,72:
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: 0510n, No. 5607849man F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-5:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA to mRNA ORIGINAL SOURCE:
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                              TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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SLECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEPHONE: (703)413-2220
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE: liver
                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOTOKI, MASAO
NAGASE, KAZUO
MATSUI, HIROSHI
VENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
VENTION: FROM FISH
2088 base pairs
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                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                   5607849man F.
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                                                                                                                                                                                                  08/004,729
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Pred. No. 27
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Best Local Similarity
Watches 19; Conserve
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                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE: CLASSIFICATION: 435
CLASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Patent No.
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/004,729

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5514573man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-599-

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                           TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2921 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22202
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: YSTEM: PC-DOS/MS-DOS
The see #1.0
             MOLECULE TYPE: c
ORIGINAL SOURCE:
ORGANISM: Ther
TISSUE TYPE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1/50 CITY: Arlington STATE: Virginia
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ORGANISM: Theragra chalcogramma
TISSUB TYPE: liver
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FEATURE:
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                                                                               TOPOLOGY:
                                                                                           STRANDEDNESS:
                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                           TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1755 Jefferson Davis Highway, Fourth Floor
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NAKANISHI, KAZUO
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1..2085
               Theragra chalcogramma
E: liver
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                                                            CDNA to mRNA
                                                                                              double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.0%;
95.0%;
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Pred. No. 27;
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US-08-164-839-9
Query Match
Best Local Similarity
"---hes 19; Conserve
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                                                                           ; LOCATION:
US-08-583-799-9
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                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENT NC compatible
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION UMBER: US/08/583,799
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Theragra chalcogramma
TISSUE TYPE: liver
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                      MOLECULE TYPE:
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CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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                                                                                                         NAME/KEY:
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5607849
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MATSUI, HIROSHI
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              Conservative
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32..2122
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95.0%;
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95.0%;
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                           Score 18.4; DB 1; Length 2921; Pred. No. 28;
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Pred. No. 2
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                Mismatches
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                Indels
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US-09-292-034-1/c
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APPLICANT: Reddy, P. Seshidhar
APPLICANT: Tikoo, Suresh
APPLICANT: Tikoo, Suresh
APPLICANT: Babiuk, Lorne
APPLICANT: Babiuk, Lorne
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
FILE REFERENCE: 293102002400
CURRENT APPLICATION NUMBER: US/09/292,034
CURRENT FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09142623
Patent No. 6337201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                 TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                  ATTORNEY/NO...Chang
NAME: Lee Chang
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 98-0
TELECOMMUNICATION INFORMATION:
TOTALECOMMUNICATION: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 34094
TYPE: DNA
ORGANISM: Porcine Adenovirus Type 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                     APPLICATION NUMBER: US/09/142,623
PILING DATE: September 10, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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MEDIUM TYPE: Diskett
                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koji YANAI et al.
788 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
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95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF ISOLATING -FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCING -FRUCTOFURANOSIDASE, AND -FRUCTOFURANOSIDASE VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                               98-0989*/LC(WMC)/144
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Pred. No. 31;
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US-09-142-623-2/c
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPEFCT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/14
FILING DATE: September 10, 1
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                       TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KOJÍ YANAI et al.
TITLE OF INVENTION: -FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF.
TITLE OF INVENTION: ISOLATING -FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCTIVE OF INVENTION: -FRUCTOFURANOSIDASE, AND -FRUCTOFURANOSIDASE VARIANT
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ORIGINAL SOURCE:
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ORGANISM:
                                                                                                                             ORGANISM:
                                                                                                                                                                                                                  LENGTH: 1905 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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LOCATION: 1 .. 788
IDENTIFICATION METHOD: E
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STRANDEDNESS:
                                                                       NAME/KEY: mat peptide LOCATION: 1 . 1905
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                                                      IDENTIFICATION METHOD:
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                                                                                                                                                                                                 Linear
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                                                                                                                            Microorganism: Aspergillus niger ACE-2-1 (ATCC 20611)
                                                                                                                                                                                  Genomic DNA
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 84.0%;
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Pred. No. 1.2e
0; Mismatches
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 Score 16.8;
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4.
Length 1905;
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; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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US-09-103-840A-1/c
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US-09-103-840A-2/c
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                                                                                                                                                                                                               TITLE OF INVENTION: DNA SEQUENCES FOR STRA:
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                             Query Match
Best Local Similarity
Matches 18; Conserv
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APPLICANT: FLEISCHAAN, Robert
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
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Matches 18; Conserva
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Best Local
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Patent No. 6294328
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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4397533
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TCACCACGGTCAGCACCGTC 4397514
                   TCACCACCGTCAGCACCTTC
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90.0%;
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0; Mismatches 2;
                                                                                Score 16.8;
Pred. No. 84;
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Pred. No. 84;
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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: ANUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ANUGUENCES FOR DIAGNOSTICS AND THERAPEUTICS
FILE, REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 828
LENGTH: 2577
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-828
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-793
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US-09-252-991A-793/c
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US-09-252-991A-828
/ Sequence 828, Application US/09252991A
/ Patent No. 6551795
Search completed: September 16, 2003, 20:42:31 Job time : 41.5446 secs
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 793
LENGTH: 2508
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: 1998-02-18
PRIOR APPLICATION NUMBER: 1598-02-18
PRIOR APPLICATION NUMBER: 1598-02-18
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                                                                                                                                                                                                                       Query Match 82.0%; Score 16.4; I
Best Local Similarity 94.4%; Pred. No. 1.99
Matches 17; Conservative 0; Mismatches
                                                                                                             1401 TCAGCACCGTCAGCACCT 1418
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
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seq length: 2000000000
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                                                                                                                                                                        Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09P_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09P_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09P_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09P_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                                                                                                                                                                IDENTITY_NUC Gapext 1.0
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20
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                             _6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
SUMMARIES
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| 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 18.4 | 18.4 | 18.4 | 20 | Score |
| 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 84.0 | 92.0 | 92.0 | 92.0 | 100.0 | Match |
| 1813 | 1691 | 1629 | 1339 | 1336 | 1336 | 788 | 585 | 498 | 498 | 466 | 84 | 34094 | 34094 | 34094 | 154746 | Query Match Length DB |
| 14 | 10 | 14 | 12 | 12 | 12 | 10 | 13 | 11 | 9 | 9 | 9 | 15 | 14 | 12 | 12 | |
| US-10-128-714-1340 | US-09-938-842A-3140 | US-10-128-714-2340 | US-10-017-161-813 | US-10-017-161-1545 | US-10-017-161-569 | US-09-990-385-10 | US-10-027-632-227474 | US-09-918-995-26919 | US-09-864-761-15233 | US-09-864-761-2089 | US-09-864-761-31756 | US-10-245-603A-1 | US-10-199-550-1 | US-09-963-038A-1 | US-09-827-688-8 | ID |
| Sequence 1340, Ap | Sequence 3140, Ap | Sequence 2340, Ap | Sequence 813, App | Sequence 1545, Ap | Sequence 569, App | Sequence 10, Appl | Sequence 227474, | Sequence 26919, A | Sequence 15233, A | Sequence 2089, Ap | Sequence 31756, A | Sequence 1, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 8, Appli | Description |

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| 5 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 |
| 15.8 | 15.8 | 15.8 | 15.8 | 15.8 | 15.8 | 15.8 | 15.8 | 15.8 | 15.8 | 15.8 | 15.8 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16.4 | 16.4 | 16.4 | 16.4 | 16.4 | 16.8 | 16.8 | 16.8 | 16.8 |
| 79.0 | 79.0 | 79.0 | 79.0 | 79.0 | 79.0 | 79.0 | 79.0 | 79.0 | 79.0 | 79.0 | 79.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 82.0 | 82.0 | 82.0 | 82.0 | 82.0 | 84.0 | 84.0 | 84.0 | 84.0 |
| 549 | 501 | 409 | 393 | 323 | 318 | 289 | 289 | 278 | 273 | 212 | 195 | 27359 | 27359 | 1918 | 1918 | 878 | 878 | 243 | 2394 | 927 | 628 | 628 | 628 | 4099 | 3812 | 2099 | 1905 |
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| US-09-864-761-12076 | US-09-867-550-1533 | US-09-864-761-4131 | US-09-878-574-1401 | US-09-878-574-2422 | US-10-040-739-741 | US-10-079-854-203 | US-09-764-878-203 | US-09-864-761-28656 | US-09-738-626-3003 | US-09-764-891-267 | US-09-864-761-20885 | US-10-281-319-3 | US-09-822-863-3 | US-10-281-319-1 . | US-09-822-863-1 | US-10-027-632-166053 | US-10-027-632-166052 | US-09-969-708-366 | US-09-815-242-4016 | US-09-815-242-6115 | US-10-027-632-289729 | US-10-027-632-289728 | US-10-027-632-289727 | US-10-128-714-5340 | US-10-128-714-340 | US-10-128-714-6340 | US-09-990-385-2 |
| Sequence 12076, A | Sequence 1533, Ap | 131 | Sequence 1401, Ap | Sequence 2422, Ap | Sequence 741, App | Sequence 203, App | Sequence 203, App | Sequence 28656, A | Sequence 3003, Ap | Sequence 267, App | Sequence 20885, A | Sequence 3, Appli | | | | | | Sequence 366, App | 4 | Sequence 6115, Ap | Sequence 289729, | | Sequence 289727, | 5340 | | 6340 | Sequence 2, Appli |

ALIGNMENTS

US-09-827-688-8/c

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RESULT 2
US-09-963-038A-1/c
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Publication No. US20030165476A1
GENERAL INFORMATION:
APPLICANT: ORSON, FRANK
APPLICANT: KINSEY, BERMA
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION DITTLE OF INVENTION: AGENTS
Sequence 1, Application US/09963038A
Publication No. US20030143200A1
GENERAL INFORMATION:
APPLICANT: Tikoo, Suresh K.
TITLE OF INVENTION: PORCINE ADENOVIRUS E1 REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 20; DB: Best Local Similarity 100.0%; Pred. No. 9.8; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: P01949US1/10004014
CURRENT APPLICATION NUMBER: US/09/827,688
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 154746
TYPE: DNA
ORGANISM: HERPESVIRUS 2
                                                                                                                                                                                                    54136 TCACCACCGTCAGCACCTTC 54117
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US-10-245-603A-1
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TITLE OF INVENTION: PORCIME ADENOVIRUS TYPE 3 GEN
FILE REFERENCE: 293102002410
CURRENT APPLICATION NUMBER: US/10/245,603A
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 09/292,034
PRIOR APPLICATION NUMBER: US 09/292,034
PRIOR APPLICATION NUMBER: US 60/081,882
PRIOR FILING DATE: 1999-04-15
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US-10-199-550-1/c
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; ORGANISM: Porcine Adenovirus Type 3
US-09-963-038A-1
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; ORGANISM: Porcine Adenovirus Type
US-10-199-550-1
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Publication No. US20030099615A1
GENERAL INFORMATION:
APPLICANT: Tikoo, Suresh K.
TITLE OF INVENTION: PORCINE ADENOVIRUS E1 AND E4 REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 34094
                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local &
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/199,550
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 09/963,038
PRIOR FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                   APPLICANT: REDDY, Police Seshidh
APPLICANT: TIKOO, Suresh Kumar
APPLICANT: BABIUK, Lorne A.
APPLICANT: BABIUK
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CURRENT APPLICATION NUMBER: US/09/963,038A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 18
                                TYPE: DNA
ORGANISM: Porcine
                    FEATURE:
                                                                          LENGTH: 34094
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19; Conserv
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Pred. No. 49
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Pred. No. 49;
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CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-08-03

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31756
LENGTH: 84
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                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 49117
OTHER INFORMATION: MAP TO AC008179.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.
OTHER INFORMATION: EST HUMAN HIT: BE891293.1, EVALUE 4.0
OTHER INFORMATION: NT HIT: L27595.1, EVALUE 1.00e-05
                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/234,687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00661
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Chen, Wensheng
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Hanzel, David K.
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Pred. No. 4:
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                                                                                                                                                              SEQ ID NO 2089
   LENGTH: 466

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRI
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
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SOFTWARE: Annomax Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                                                                                    FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/234,687
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APPLICATION NUMBER: PCT/US01/00661
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                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00670
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0. US20020048763A1
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Chen, Wensheng
                                                                                                                                                                                                                DATE:
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l, David K.
MAP TO AC009303.1
EXPRESSED IN ADULT LIVER, SIGNAL =
EXPRESSED IN HEART, SIGNAL = 0.86
EXPRESSED IN BRAIN, SIGNAL = 1.2
EXPRESSED IN BONE MARROW, SIGNAL :
                                                                                                                                                                                                                                                                                                                      2001-01-30
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Pred. No. 2.4e
0; Mismatches
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Query Match
Best Local Similarity
Thes 18; Conserve
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PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                    SOFTWARE: Annomax
SEQ ID NO 15233
LENGTH: 498
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Best Local S
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Patent No. US20020048763A1
                                                                                                                                    TYPE: DNA
ORGANISM: Homo :
FEATURE:
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PRIOR
PRIOR
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 49117
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                                                                                                   OTHER INFORMATION:
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APPLICATION NUMBER: PCT/US01/00669
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Chen, Wensheng
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Rank, David R.
Hanzel, David K.
                                                                                                                                                                                                                                                           DATE:
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                                                                                                   MAP TO AC008179.1
EXPRESSED IN FETAL LIVER,
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                                84.0%;
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                Score 16.8; Di
Pred. No. 2.5e
0; Mismatches
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.Pred. No. 2.5e+02;
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                                                                                                                                                                                                                       Engine
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                                .5e+02
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                                                Length 498;
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Conservative

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Gaps

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APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES

FILE REPERENCE: 2041-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR PILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOPTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 26919
                                                                                                                                                                                                                                                                               APPLICANT: WANGE, David G.
APPLICANT: WANGE, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERRENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/6/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR APPLICATION NUMBER: US 60/167,363
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; LCATION: (1)...(498)
OTHER INFORMATION: n = A,T,C or
U9-09-918-995-26919
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US-09-918-995-26919/c
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                                              ; ORGANISM: Human US-10-027-632-227474
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Publication No. US20030073623A1
GENERAL INFORMATION:
Query Match
                                                                                                                    NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 227474
LENGTH: 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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90.0%;
84.0%;
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Pred. No. 2.5e+02;
Score 16.8;
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  DB 13;
Length 585;
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RESULT 11
US-10-017-161-569
; Sequence 569, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
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US-09-990-385-10/c
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                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: KOji YANAI et al.

APPLICANT: KOji YANAI et al.

TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF

ISOLATING BETA-FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCI

BETA-FRUCTOFURANOSIDASE, AND BETA-FRUCTOFURANOSIDASE VARIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/990,385
FILING DATE: 10-Sep-1998
FILING DATE: 10-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/142,623
FILING DATE: September 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                772 TCTCCACCGTCTGCACCTTC 753
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                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Microorganism: Aspergillus niger ACE-2-1
. (ATCC 20611)
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 788 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 40,949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                                                                      84.0%;
90.0%;
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Pred. No. 2.
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PPLICANT:

ABURATANI, HIROYUKI

akiyama,

KIYOSHI MA, YUTAKA

SUWA, MAKIKO

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RESULT 12
US-10-017-161-1545
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1545, Application US/10017161 Publication No. US20030143668A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                        APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
IEQ ID NO 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SUWA, MAKIKO APPLICANT: ASAI, KIYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 084335/0152
                                                   10-017-161-1545
                                                                                                                                                                      PEATURE:
NAME/KEY: source
LOCATION: (1)..()
                                                                NAME/KEY: CDS
LOCATION: (785)..(1136)
                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (78)
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                                                                                                     FEATURE:
                                                                                                                                       NAME/KEY: CDS
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                                                                                                                                                                                                                                                            ENGTH: 1336
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90.0%;
84.0%;
90.0%;
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Pred. No. 2
Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1336;
                Length 1336;
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APPLICANT: Tishkott, Daniel Applicant: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
ITILE OF INVENTION: Jeentification of Essential Genes in Aspergillus fumigatus and
ITILE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR PRICING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
NUMBER OF SEQ ID NOS: 8603
NUMBER OF SEQ ID NOS: 8603
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GENERAL INFO...

APPLICANT: Jiang, BO
APPLICANT: Hu, Wengi
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Identification
APPLICANT: Lemieux, Gebastien M
APPLICANT: Lemieux, Gebasti
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Best Local Similarity
Matches 18; Conserv
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NAME/KEY: SOUTCE
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CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
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TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
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APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIRO
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ORGANISM: Homo sapiens
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Sequence 3140, Application US/09938842A

Patent No. US20020160378A1

Patent No. US20020160378A

PAPPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

PATENCOF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

PILE REFERENCE: SCRIP1300-3

CURRENT PAPLICATION NUMBER: US 60/29/938,842A

CURRENT PAPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR PILLING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR PILLING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 3140

LENGTH: 1691

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-3140
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; LENGTH: 1629
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-2340
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Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
                                                                                                                                                  Brassica oleracea

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.

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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea
Unpublished
Other_GSSs: BOMBH09TR
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RESULT 3
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaceae; Brassica.
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DNA is from a doubled)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-838-3523
Fax: 301-838-0208
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Town, C.D., van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
a 134 c 200 g 220 t
                                                                                                                                                                                                                                                                                                                                                        genomic DNA inserted into \overline{p}HOS1 using 92 c 126 g 125 t
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/mol_type="genomic DNA"

/strain="TO1000DH3"

/db xref="taxon:3712"

/clone="BOHHM39"
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Pred. No. 3.3e+02;
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BOHHM39, genomic
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AU291667
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Best Local S
Matches 19
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                                                                                                                                     AU291667 zinnia cultured mesophyll cell equalized elegans cDNA clone Z6332, mRNA sequence.
AU291667 ZINDIA clone Z6332, mRNA sequence.
AU291667 ZINDIA CLONE Z6332, mRNA SEQUENCE.
Zinnia elegans
Zinnia elegans
Zinnia elegans,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
asterids, campanulids, Asterales, Asteraceae, Asteroideae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

plate: 399 row: M column: 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BZ201556
471 bp DNA linear GSS 11-OCT-200: CH230-399M1.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-399M1, genomic survey sequence.
BZ201556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shv, A., Gebregeorgis, C., Overton, L., Russell, D., Chen, D., Ri
Jong, P. and Fraser, C., M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: T7
Class: BAC ends.
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Other_GSSs: CH230-399M1.TJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BZ201556.1 GI:23859608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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/note="Vector: pTARBAC1.3; Site_1: MboI; Site_CHOR1-230 Rat (BN/SsNHad/MCW) BAC library prodeficter de Jong"
a 128 c 116 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/mol types"genomic DNA"
/strain="BN/SsNHsd/MCW"
/db xrefs="taxon:10116"
/clone="CH230-399M1"
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95.0%;
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Pred. No. 1.3e+03;
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duced by
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Heliantheae; Zinnia.

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BM619819/c
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19; Conserv
                                                                                                                                                                                                                                                                                            1 (bases 1 to 563)
Holt,R.A., Lin,J.-J., Murphy,S.D.,
R., Collins,F.H., Venter,J.C. and
                                                                                                                                                                                                                                                                                                                                                                      Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EST.
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                                                                                                                                                                                            45 w. Gude Dr., Rockville, Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM619819.1 GI:18918237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17000687440937 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone 19600449618554 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: demura@postman.riken.go.jp
This clone was obtained at our laboratory.
Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 81-45-503-9605
Fax: 81-45-503-9573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN Plant Science Center
1-7-22 Suehirocho, Yokohama, Kanagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Taku Demura
Morphogenesis Research Group
                                                                                                                      Plate: NU01004N8H row: H
Seq primer: M13 Reverse.
                                                                                                                                                                                                                               Celera Genomics
                                                                                                                                                                                                                                              Contact: Holt R.A.
                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                               Celera Anopheles gambiae
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            /organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc.
chromosome)"
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/clone_Tib="zinnia_cultured mesophyll cell equalized cDNA"
/note="Vector: pGEM-T easy; cultured in tracheary element differentiation-inductive medium"
158 c 90 g 105 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zinnia elegans"
/mol_type="mRNA"
/cultivar="Canary bird"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
db_xref="taxon:7165"
                                                                                                     ocation/Qualifiers
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Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                  Evans, C.A., Kraft, C.L., Charlab Hoffman, S.L.
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Best Local :
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Best Local
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Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celera Genomics
45 w. Gude Dr., Rockville,
Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17000659210616 A.Gam.ad.cDNA.blood1 19600447014826 5', mRNA sequence. BM57514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
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Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                          Email: HoltRA@celera.com
Plate: NU01003SIT row: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Celera Anopheles gambiae EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles.

1 (bases 1 to 568)
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 2404534580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult morguitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
                                                                             /note="Weettor: pSport1; Site 1: Sal1; Site 2: Not1; Who adult mosquitoes (mixed sex) frozen on liquid nitrogen hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org) 139 c 136 g 118 t
                                                                                                                                                                                                                                                                                   /organism="Anopheles gambiae"
/mol type="mdNA"
/strain="RSP-ST (Reduced susc.
.stromosome)"
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/dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                      dev_stage="Adult"
lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                      clone_lib="A.Gam.ad.cDNA.blood1"
                                                                                                                                                                                                                                                                       db_xref="taxon:7165"
                                                                                                                                                                                                                                                       clone="19600447014826"
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95.0%;
                 92.0%;
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                 Score 18.4; DB 17
Pred. No. 1.3e+03
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                                                                                                   (www.malaria.mr4.org)"
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                               Length
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                                   568;
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1 TCACCACCGTCAGCACCTTC

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COMMENT
                                       RESULT 8
BM635604/c
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                                                                                                                                                                                                                         Query Match
Best Local (
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                                                                                                                           211
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Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
1 (bases 1 to 574)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
R. Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
BM635604 625 bp mRNA linear EST 26-FEB-2002 17000687558989 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
                                                                                                                                                              1 TCACCACCGTCAGCACCTTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simon Hubbard
Department of Biomolecular Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU374492 574
603813877F1 CSEQCHN74 Gallus
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                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PO Box 88, Manchester,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12445392
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                                                                                                                                                                                                                                                                                                /note=Worgan: kidney + adrenal; Vector: pBluescript II
KS(+), Site 1: EcoRI; Site 2: Not1; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to Not1 adapters, digested with EcoRI
, size-selected, and cloned into the Not1 and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1995; 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simon. Hubbard@umist.ac.uk.
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/mol_type="mRNA"
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/db_xref="taxon:9031"
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                                                                                                                                                                                                                         92.0%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lib="CSEQCHN74"
                                                                                                                                                                                                      0
                                                                                                                                                                                                                         Score 18.4; DB 13; Pred. No. 1.4e+03;
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gallus
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Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryg
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
                                                                                   1 (bases 1 to 635)
1 (bases 1 to 635)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
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Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A.,
,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
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Tel: 2404533151
Fax: 2404534580
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Contact: Holt R.A.
                                         Celera Genomics
                                                              Contact: Holt R.A.
                                                                                 Unpublished
                                                                                                                                                                                   Anopheles.
                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
1 167 c 180 g 138 t
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/strain="RSP-ST (Reduced susc.
chromosome)"
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/lab_host="DH10b"
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/clone="19600449658640"
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95.0%;
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A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
5', mRNA sequence.
                       Rockville,
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Pred. No. 1.4e+03;
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EST 26-FEB-2002

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Gaps

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RESULT 10
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                                                                                                                                                         Seg primer. ...
Class: sheared ends.
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Email: HoltRA@celera.com
Plate: NU01004N8F row: P
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                 Tel: 301-838-3523
                                                                                                                                                                                                                                                                                                9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                   Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                   Other_GSSs: BOMGX07TF
                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 658)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea
Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence
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                                                                                                                                                                                                                              Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                 Whole genome shotgun sequencing of Brassica oleracea
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/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
/Clone lib="BO 2 3 KB"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 211 c 142 g 151 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="19600449617587"
/dev_stage="Adult"
/lab_host="DH10b"
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/mol_type="mRNA"
                                                                                                          organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
                                                                                           db_xref="taxon:3712"
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17000687312069 A.Gam.ad.
19600449707650 5', mRNA
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Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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17000687440855 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449618598 5', mRNA sequence.
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EST.
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Seq primer: M13 Reverse
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Fax: 2404534580
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Anopheles gambiae (African malaria mosquito)
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45 w. Gude Dr., Rockville,
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/clone="19600449618598"
/dev_stage="Adult"
/lab_host="DH10b"
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/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
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/mol_type="mRNA"
/strain="RSP-ST (Reduced susc
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Pred. No. 1.4e+03;
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Contact: Holt R.A.
Celera Genomics
45 w. Gude Dr., Rockville, M
Tel: 2404533151
Fax: 2404534580
                                                                                                                                                  1 (bases 1 to 687)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., R., Collins,F.H., Venter,J.C. and Hoffman,S.L. Celera Anopheles gambiae EST project
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17000687326166 A.Gam.ad.cDNA1 Anopheles gambiae
19600449658826 5', mRNA sequence.
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               Email: HoltRA@celera.com Plate: NU01004HNI row: F Seq primer: M13 Reverse.
                                                                                                                                                                                                                                    Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Holt,R.A., Lin,J.-J.,
,R., Collins,F.H., Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 w. Gude Dr., Rockville, Tel: 2404533151
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/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mesquitoes (mixed sex) Frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)" a 158 c 232 g 112 t
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/mol type="mRNA"

/strain="RSP-ST (Reduced susc.
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Indopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                           GI:18948051
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Pred. No. 1.4e
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VERSION
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BZ158304
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BZ158304 704 bp DNA linear GSS 11-OCT-200 CH230-387I4.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-387I4, genomic survey sequence.
                                                                                                                                                                                                                                                                        Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 387 row: I column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other GSSs: CH230-38714.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., Ough, P. and Fraser, C.M.
Rat, BAC End Sequences from Library CHORI-230 MboI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinas;
                                                                                                                                                                                                                               Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BZ158304.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3', Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome)
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/lab_host="DH10b"
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/strain="RSP-ST (Reduced
                                                                                                    /mol_type="genomic DNA"
/strain="BN/SBNH8d/MCW"
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/clone="19600449658826"
                                              /clone="CH230-38714"
                                                                          /db_xref="taxon:10116"
                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                   ocation/Qualifiers
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cell_type="Brain"
                              /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:23799259
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Pred. No. 1
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BASE COUNT
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AUTHORS
TITLE
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CD261546
LOCUS
DEFINITION
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Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
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     693
74
                                                                 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and propagation
Unpublished
Contact: Tyler B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 712)
Tyler, B.M., Judelson, H.S., Gijzen, M., Dean, R.A. and Waugh, M.E.
USDA-IFAFS: Expression of Phytophthora sojae genes during infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phytophthora sojae
Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD261546 712 bp mRNA linear EST 23-MAY-2003 psmA012XO15f 189662 sMA: Phytophtora sojae grown in synthetic medium Phytophthora sojae cDNA clone sMA012O15 5, mRNA sequence CD261546
                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 712.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          FORWARD: BK reverse Plate: 012 row: O column: 15 Seq primer: BK reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                        1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtyler@vt.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD261546.1 GI:31049373
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                          PCR PRimers
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                                                                                                                                                                          /tissue type="mycelium"
/cell_lIne="P6497"
/dev_Stage="mycelium"
/clone_lib="sMA: Phytophtora sojae grown in synthetic
medium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SsNHsd/MCW) BĀC library produced by
Pieter de Jong"
171 c 204 g 173 t
                                                                                                                                            /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: xhoI" 203 c 213 g 124 t
                                                                                                                                                                                                                                                           /organism="Phytophthora Bojae"
/mol_type="mRNA"
/db_xref="reaxon:67593"
/clone="sMA012015"
                                                                              92.0%;
95.0%;
                                                              Score 18.4; DB 14;
Pred. No. 1.4e+03;
0: Mismatches 1;
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                                                                                             Length 712;
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Search completed: September 16, 2003, 20:39:49 Job time: 1016.28 secs

BEST MAILABLE CORY